

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:27:32 ; Search time 44 Seconds
(without alignments)
1431.942 Million cell updates/sec

Title: US-10-663-157-2

Perfect score: 3456
Sequence: 1 MGTPSSSTALASCRIARR.....SQEASOTLDSVYSHLPDLL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2350	68.0	651	2 JC7705	death receptor-6 -
2	343.5	9.9	461	1 A5336	tumor necrosis fac
3	275.5	8.0	459	2 I48854	gene murine tumor
4	273.5	7.9	474	2 B38634	tumor necrosis fac
5	236.5	6.8	416	1 JN0006	nerve growth facto
6	235.5	6.8	255	2 I38426	lymphocyte activat
7	233	6.7	305	2 A46476	B cell-associated
8	228.5	6.6	435	2 I34182	tumor necrosis fac
9	218.5	6.3	326	1 GOVZML	T2 protein - myxom
10	211.5	6.1	325	2 B43692	T2 protein - rabbi
11	211.5	6.1	425	1 A26431	nerve growth facto
12	210.5	6.1	427	1 GGHUN	nerve growth facto
13	206.5	6.0	348	2 T28623	hypothetical prote
14	206.5	6.0	349	2 D36858	gene G4R protein -
15	205	5.9	595	2 A42086	C530 antigen precu
16	204.5	5.9	349	2 D21715	G2R protein - vari
17	200	5.8	277	2 A60771	B-cell activation
18	193	5.6	461	2 J43052	tumor necrosis fac
19	191.5	5.5	2824	2 T22759	hypothetical prote
20	187.5	5.4	493	2 J5496	membrane glycoprot
21	186.5	5.4	461	1 GQRTT1	tumor necrosis fac
22	180.5	5.2	256	2 B32393	T-cell antigen 4-1
23	170	4.9	454	1 GQMT1	tumor necrosis fac
24	154	4.5	277	2 I37552	OX40 homolog - hum
25	148	4.3	271	2 T32783	OX40 antigen precu
26	145.5	4.2	455	1 GGHUT1	tumor necrosis fac
27	142.5	4.1	1193	2 A44018	laminin B2t chain
28	138	4.0	1827	2 T34288	hypothetical prote
29	136.5	3.9	1205	2 T27053	hypothetical prote

30	136.5	3.9	1372	2 T25933	hypothetical prote
31	136	3.9	272	2 I49700	gene ox40 protein
32	135.5	3.9	5376	2 T42215	zonadhesin - mouse
33	132.5	3.8	1252	2 S35016	oocyst wall protei
34	129.5	3.7	3570	2 T45025	mucin MUC5B, trach
35	129	3.7	1459	2 T30196	kinesin motor prot
36	128.5	3.7	634	2 T00388	hypothetical prote
37	128.5	3.7	987	2 I48652	mouse developmenta
38	128.5	3.7	1032	2 T34433	hypothetical prote
39	128.5	3.7	2232	2 T34434	hypothetical prote
40	127.5	3.7	987	2 I48953	eph-related recept
41	126	3.6	1440	2 T27942	lin-15B protein -
42	125.5	3.6	1379	1 S01254	hepatocyte growth
43	123.5	3.6	557	2 A48434	variant-specific s
44	123.5	3.6	1367	1 S48478	glucan 1,4-alpha-g
45	123	3.6	2183	2 T42764	coagulation factor

ALIGNMENTS

RESULT 1

JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C:Accession: JC7705
R:Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705, MUID:21308433, PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.
C:Genetics:
A:Gene: dr-6
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: Ovary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F:332-350/Domain: transmembrane #status predicted <TM>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 68.0%; Score 2350; DB 2; Length 651;
Best Local Similarity 70.6%; Pred. No. 5.8e-148;
Matches 459; Conservative 47; Mismatches 102; Indels 46; Gaps 10;

QY	23	ATMIAGSILLGLFLSTTAQP----	EOKASNL-IGTYRHVDATGQVLTCDKCPAGTVYS	77
DB	3	AAVLAALVLLVFLVFGADAPQLT	BEQNAVSLPAGKYLHLDRTNQELICDKCPAGTVYS	62
QY	78	EHCITNTSLRVCSCFVGTFTRHENGIEKCHDCSQCPMPMIKLP	CAALTDRECTCPGM	137
DB	63	KHCTKSTLRBCSPCDGTTTKHENGIERCHPCKECELP	MIKTHCTALTDRCTCLSGT	122
QY	138	FQSNATCAHTVCPVGVGRKXGTETEDVRQCQARGTFSDVPSSVMKCA	YTDCLSQL	197
DB	123	FQINDTCVETVCPVGVGRKXGTETEDVRCKPCLRGTFSDVPSSVMKCT	YTDCTFCGKM	182
QY	198	VWIKPTKTDNVC----	GLTP--SPSSSTSRSPGGTAIPRPEHMETHEVPSSTYVPKGMN	252
DB	183	VVVKPTKESDNCVKSPLNTSLTSSDAQDG-----	ETYEAPPTAYLPKGLN	232
QY	253	STESNSASVRPRKVLSSIQEGTVDPNTSSARGKEDVNKTL	PNLVQVNHQGGPHRHILKL	312
DB	233	SSVFDLSSFPAPRVSNGTAEPTVDYNDTANGTVGAPGSL	SAGTAGAQSQVSRHKHTSOA	292
QY	313	L----	PSMEATGCKSPTPIKGRGHPRONLKHHPDINEHLPMLVFLVLLVIVVCS	369

A;Residues: 1-22 <XIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1.; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homologous domain
C;Keywords: cytokine receptor; transmembrane protein
E;1-22/Domain: signal sequence #status predicted <SIG>
E;23-47/Product:tumor necrosis factor receptor type 2 #status predicted <MAT>
E;48-77/Domain: NGF receptor repeat homology <NG1>
E;79-120/Domain: NGF receptor repeat homology <NG2>
E;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 7.9%; Score 273.5; DB 2; Length 474;
Best Local Similarity 25.0%; Pred. No.1.5e+10;
Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;

Qy 65 LTCDKCPAGYVSHCHNTSLRVCSGSPGVGFTHENGIEKCHDCSDCPMPWMIKKLPDCA 124
Db 53 MCCAKCFPGGYVKHFCKNTCTDTVCADCEASMYTVMNQFTCLSCSSSTTTDVVEIRACT 112
Qy 125 ALTDRECTCPGFMFSNAT-----CAPHTVCPVGWGVRKKGTETEDVRKCQCARGTF5 177
Db 113 KQNHRVACACAGRYCALKTHTSGRCQCVRLSKCGFGFGVASSRAPNGVNLCACAFGTF5 172
Qy 178 DVPSSVMKKAYTDCLSQLNVIVIKPKTKETDNVCGTLPSFFSSTSPPSGTAIFPRPEHME 237
Db 173 DTTSSTDVCRPHRIC----SILAIPGNASTDAVCA-----PESPT 208
Qy 238 THEVPSSTYV----PKGWNTESSNSASVPRKVLLSSIQEIGTVPDNTSSARKEDVNKTLTP 293
Db 209 LSAIPRTLYVSQEPETRSQLDPBGSQTPTSILTSL--GSTPIEQSTKG---GISLP 262
Qy 294 -----NLQVVN-----HOQGPH-----HRHLTK 311
Db 263 IGLIVGVTSGLMLGLVNCIILVQRKKPSCLODKAPVHPVDEKSQDAVLGEQOHLT 322
Qy 312 LLRSMETATGEEKST--PIKPGRKEGHR 337
Db 323 TAPPSSSSSSLESSASAGRRAPEGHQ 350

RESULT 5
JN0006

Nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Wesskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reissman, P.M.
Neuron 2, 1123-1134, 1999
A;Title: Structure and developmental expression of the nerve growth factor receptor in chick embryo neurons.
A;Reference number: JN0006; PMID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fteimie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; PMID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells and on Schwann cells. The cysteine-rich region of the extracellular domain may form part or all of the binding site for nerve growth factor.
C;Comment: This protein is thought to form a high-affinity receptor when it associates with p75^{NTR}.
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
E;1-20/Domain: signal sequence #status predicted <SIG>
E;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>

F:141-181/Domain: NGF receptor repeat homology <NG4>

F:189-237/Region: serine/threonine-rich

F:240-261/Domain: transmembrane #status predicted <MEM>

F:262-416/Domain: intracellular #status predicted <INT>

F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 236.5; DB 1; Length 416;

Best Local Similarity 23.2%; Pred. No. 3.7e-08;

Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;

QY 67 CDKCPAGTVVSEHCNTSLRYCSSC-PVGTFRHENGIEKCHDCSQCPMPMIEKLPCAA 125

Db 36 KCACNLGGVQPC-GVNTQCEPCLDSVTYSDVSATEPKCKTQ-CVGLHSMSPCVE 93

QY 126 LTDRCTCPGPMFQS--NATCAPHTVCPVGVGRKKTETEDVRCKOCARGTSDVPSSV 193

Db 94 SDDAVCRCAVGYFQDELJSGSKESICEVGFGLMFPQCDSDQTVCECPGEGTDEANFV 153

QY 184 MKCKAYTDCLSNLVVIKPGTKETDNVCGTL-----PSFSSSTSPSPGTAFPRPEH 235

Db 154 DPLCLPTIC-BENEMVKECTATDAECRLHPRWTHTFSLAGSDSPETIRDPNTEG 212

QY 236 MATHVPSSTVYKGMSTENSSAS-----VRPKVLSIOEGTVDPDNTSSARGKEDVNKT 291

Db 213 MATTLADIVTTVMGSSQPVSRGTADNLIPYCSILAAVVGLVAYIAFRWNSCKQNKQ 272

QY 292 LPNLQVNVHQGPHRHILKLLPSMEATGGKSTPIKPKRGHPRONLKHDFDNEHLP 351

Db 273 GANRPVNTSPSE-----GEK-----LHSDSGI----- 236

QY 352 WMIVLFLVLLVVIIVCSIRKSRRLKGPQDPSAIVEK--AGLKKSMTPTONRKWIY 409

Db 297 -----SVDQSLLHQDPFNQSTQGPAPKGDGLYASLPSPKQEE----- 335

QY 410 YCNHGIDILKLVAAQVGSQKDIYQFLCNASEREVAFNSGY-----TADHERAYA 461

Db 336 -----VEKLSSASAEETWRQL-----AGELGYKEDLIDCFTEESPARA 374

QY 462 ALQHWITRGPRASLAQLISALRQHRNDVVEKI 494

Db 375 LLADWSAK-ETATLDALLVALRKIQRGDIABSL 406

RESULT 6

I38426

Lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000

C:Accession: I38426; JT0752

R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R

Sur, J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434; PMID:8088337

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <RES>

A:Cross-references: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne

A:Reference number: JT0752; MUID:94085794; PMID:8262389

A:Accession: JT0752

A:Molecule type: mRNA

A:Residues: 1-106, R', 108-255 <SCH>

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro

C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F:187-213/Domain: transmembrane #status predicted <TM>

F:136,149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 6.8%; Score 235.5; DB 2; Length 255;

Best Local Similarity 30.4%; Pred. No. 2.3e-08;

Matches 63; Conservative 24; Mismatches 77; Indels 43; Gaps 8;

QY 25 MIAGSLLGLSTTAQPEQKASNLICTYRHVDRATQVLTCDKCPAGTVVSEHCNTS 84

Db 8 IVATLLLVNLFERTSLQD-----PCNCPAGTF-----CDNRR 41

QY 85 LRVCSGPCVGTFRHENGIEKCHDCSQCPMPMIEKLPAAALTDRECTPPGPMFQSNATC 144

Db 42 NQICSPCPNFS-SAGGRTCDICRQ--CKGVFRTRKCSSTSNABCDCTGPFHCLGAGC 99

QY 145 AP-HTVCPVGVGRKKTETEDVRCKOCARGTSDVPSSVMKCKAYTDCLSNLVVIKPG 203

Db 100 SMCEQDCQGGQELTKG-----CKCCFGTFNDQKRGI--CRPWTNCSLDGKSVLVNG 150

QY 204 TKETDNVCGTLPS-----FSSSTSPSP 225

Db 151 TKERDVVCGSPADLSPGASSVTTPAP 177

RESULT 7

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A:Reference number: A46476; MUID:92105763; PMID:1370315

A:Accession: A46476

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; NID:g1553058

A:Note: sequence extracted from NCI backbone (NCBIN:75206, NCBIP:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,

J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586; PMID:1281194

A:Accession: A46515

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV', <GRI>

A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N

A:Experimental source: BAUB/C, liver

A:Note: sequence extracted from NCI backbone (NCBIP:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46476.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 6.7%; Score 233; DB 2; Length 305;

Best Local Similarity 34.9%; Pred. No. 4.2e-08;

Matches 53; Conservative 21; Mismatches 70; Indels 8; Gaps 4;

QY 67 CDKCPAGTVVSEHCNTSLRYCSSCPVGTFRHENGIEKCHD---CSQCPMPMIEKLPC 123

Db 38 CULQCGRLTSHCTALEKTCQHPDCDSGEFAQWNRREIRCHQHRHC-EPNQLAVKK-EG 95

QY 124 AALTDRECTPPGPMFQSN---ATCAPHTVCPVGVGRKKTETEDVRCKOCARGTSDVP 180

Db 96 TAESDVTCTCKEGQCHTCKDCBACAHQTPCIPGFGVEMEMATETDITDVTCHPCVPVFFNSQS 155

QY 181 SSMKCKAYTDCLSNLVVIKPGTKETDNVCG 212

Db 156 SLFEKCYPTWSCEDKNLEVLQKGTQTNVICG 187

RESULT 8

I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequences
A:Reference number: I54182; MUID:93252381; PMID:8486360
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:I04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.6%; Score 228.5; DB 2; Length 435;
Best Local Similarity 30.9%; Pred. No. 1.3e-07;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPC-PWPMEIKL-P 122
DB 57 ICCSRCPGTYVSXKSRIRDTVCATCAENSYNEHWYLTICQLC-RPCDPVWGLEIAP 115
QY 123 CAALTDRECTCPGQFQSNATCAHTV-----CPVGVGRKKGTETE----- 164
DB 116 CTSKSKTKTCRCQPGMF-----CAAWALECTHCELSDCP-----PGTEAEKDEVGKG 163
QY 165 DYRCQKQARGTSDVPSSVMKCKAYTDCLSQNLVVKGTETDNVCGT-----LPSRSS 220
DB 164 NNHCVPCKAGHQNTSSPSARCPQHTRCENQGLVEAEGTAQSDTTCNPLEPLPPMSG 223
QY 221 T 221
DB 224 T 224

RESULT 9

QVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 15-Sep-2003
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor
A:Reference number: A40566; MUID:91335768; PMID:1651597
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 218.5; DB 1; Length 326;
Best Local Similarity 36.8%; Pred. No. 4.2e-07;
Matches 50; Conservative 10; Mismatches 69; Indels 7; Gaps 2;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPC-PWPMEIKLPCA 124
DB 38 LCCTSCPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGCTGHLSESQSCD 97
QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGVGRKKGTETEDVRCKQCARGTFS 178

DB 98 KTRDRVCDCCAGNYCLLKGGGCRICAPKTKCAGYGV-SGHTRTGDVLTCKCPRTYSD 156
QY 179 VPSSVMKCKAYTDCLS 194
DB 157 AVSSTETCTSSFNYS 172

RESULT 10

B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103; PMID:2820128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 6.1%; Score 211.5; DB 2; Length 325;
Best Local Similarity 36.7%; Pred. No. 1.2e-06;
Matches 47; Conservative 7; Mismatches 67; Indels 7; Gaps 2;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPC-PWPMEIKLPCA 124
DB 38 LCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGCTGHLSESQPCD 97
QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGVGRKKGTETEDVRCKQCARGTFS 178
DB 98 RTHDRVCSNTGNYCLLKGGGCRICAPKTKCAGYGV-SGHTRTGDLTCKCPRTYSD 156
QY 179 VPSSVMKC 186
DB 157 SLSPTERC 164

RESULT 11

A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R:Metzsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoi
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <NET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Genetics: 20/3
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 211.5; DB 1; Length 425;
Best Local Similarity 22.9%; Pred. No. 1.7e-06;
Matches 119; Conservative 59; Mismatches 196; Indels 145; Gaps 25;

QY 12 ASCSRIARRATMIAGSLILGLSTTTAQPEQKASNLIGTYRHVDRAQTQVLTCDKCP 71
DB 6 AACSAIDL-----RLILLLILGVSSGGAKETCST--GLYTH-----SGE--CCKACN 49

QY 72 ACTYVSEHCNTSLRVCCSPVG-TFTREHNGIEKCHDCSPCPWPMIEKLPCLALTDRE 130
DB 50 LQEGVAQPC-GANQTVCEPCLDNVTFSDWSATEPCKPCTE-CLGLQSMSPAPCVADDAV 107

QY 131 CTCPPGMFOSNAT--CAPHTVCPVGMGVKKGTEDEVCKOCARGTFSDVPSSVMKCKA 188
DB 108 CRCAVGYQDETHGCEACSVCEVSGGLVFCQDQKQNTVCECEPGIYSDANHVDFCLP 167

QY 189 YTDCLSNLVLWIKPGTKTDNVCGTLPSFSSSTSPSPGTALPPREHMETHEVPSSTVVP 248
DB 168 CTVC-EDTERQLRETPWADABCEBIPG-----RWIPRST-PP 203

QY 249 KCMNST-ENSSASRPVKLSIQEGTVPDNTSSARGEDYKNTLPNLQVNVHQGPHR 307
DB 204 EGSSTAPSTQEPFEPPE--QDLVSTVADVMVTVWG----- 238

QY 308 HILKLLPSMEATGKSKSTPIKGRGHPRQNLHKHFDINELHFMVILFLLVLVIVW 367
DB 239 -----SSQPV--VTRG-TTDLN-----IP-VYCSILAAVAVGLV 268

QY 368 CSIR-----KSSTLKGPRQPSAIVKAGLKKSTTPQNKREKTYTTCNGHGIILKVA 423
DB 269 AVYAFKRMNSCKQKQANSRP-----VNQTPPEGEK-LHSDSGISVDSQSUDH 317

QY 424 AQVGSQWK-----DIYQFLCNASREVAFNGYVADH---ERAY----- 460
DB 318 QQTHQTASGQALKGDGNYLSSPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTH 377

QY 461 -----AALQHTWTRGPEASLAOLISALRQHRNDVVEKI 494
DB 378 ACPVRALLASWGAQ-DSATLDALLAALRIQRADIVESL 415

RESULT 12

GQHUN
nerve growth factor precursor, low affinity [validated] - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:G189204; PIDN:AAB59544.1; PID:G189205
R;Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schattteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A;Reference number: A60204; MUID:87085574; PMID:3025363

A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31, 'T', '33-42, 'TT', '45-46, 'TX', '50-51, 'XX', '54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleot
R;Visavajjhal, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:G189206; PIDN:AAA36363.1; PID:G189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; p
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 210.5; DB 1; Length 427;
Best Local Similarity 22.8%; Pred. No. 2e-06;
Matches 116; Conservative 58; Mismatches 204; Indels 131; Gaps 22;

QY 21 ATATMIAGSILLGLSTTTAQPEQKASNLIGTYRHVDRAQTQVLTCDKCPAGTYVSEHC 80
DB 5 ATGRMDGPRLLILLGLLVSLGKAECAP-TGLYTH-----SGE--CCKACNLGEGVAQPC 57

QY 81 TNTSLVCSGC-PVGTFTREHNGIEKCHDCSPCPWPMIEKLPCLALTDRETCPPGMPQ 139
DB 58 -GANQTVCEPCLDSVTFSDWSATEPCKPCTE-CVGLQSMSPAPCVADDAVCRCAVGYQ 115

QY 140 SNAT--CAPHTVCPVGMGVKKGTEDEVCKOCARGTFSDVPSSVMKCKAVTDCLSQNL 197
DB 116 DETTGCEACRVCAGSLVFCQDQKQNTVCECEPGIYSDANHVDFCLPCTVC-EDTE 174

QY 198 VWIKPGTKETDNVC-----GTLPSFSSSTSPSPGTALPPREHMETHEVPSSTV 247
DB 175 RLQRECTRWADABCEBIPKGRWTRSTPPEGSSTAPST-----QSPPEAPPEQDLASTVA 229

QY 248 PKGMNSTENSSASVPK-----VLSICEGTVPDNTSSARGEDYKNTLPNL 295
DB 230 --GVTVTVMGSSQPVVTRGTTNLPVYCSILAAVAVGLVAVYAFKRMNSCKQKQANS 287

QY 296 QVNVHQGPHRHILKLLPSMEATGGEK--SSTPIKGRGHPRQNLHKHFDINELHFM 353
DB 288 RPNVQTPPEP-----GKLLHSDSGISVDS-----QSLH---DQPH---- 320

QY 354 IVFLFLLVLVIVVCSIRKSRRLTKGPRQDPSAIVKAGLKKSTTPQNKREKTYTTCNG 413

Db 321 -----TQTASQALKG-----DGLYSLPPAKREE----- 346
Qy 414 HGIDILKLVAAQVSQWKDIYQFLCNASERVAFSNGYTAADHERAY-----AALQH 465
Db 347 -----VEKLINGSAGDTWHL-----AGELGYQPEH:DSFTHEACPVALLAS 389
Qy 466 WTIRGPEASLAQLISALRQHRNDVVEKI 494
Db 390 WATQ-DSATLDALLAALRIQADLVESL 417

RESULT 13

T28623
Hypotheical protein G2R - variola major virus
C:Species: variola major virus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C:Accession: T28623
R:Massung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60933.1; PID:G439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 6.0%; Score 206.5; DB 2; Length 348;
Best Local Similarity 34.1%; Pred. No. 2.9e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;
Qy 65 LTCDCPCAGTYVSEHCTNTSLRVSCSPVGTFTTRHENGIEKCHDCSPCPWPMIEKLPCA 124
Db 41 LCCLSCPPTGYASRLCDSKNTQCTPCGSGFTSRNNHLPACLSGRCNSNQVETRSCN 100
Qy 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGWVKRGKTETEDVRCKQCARGTFSD 178
Db 101 TTHNRICEPSFGYICLLKSGSCKACVSTQKCGIGYV-SGHTSVGDVICSFGFGTYSH 159
Qy 179 VPSSVMKCK 187
Db 160 TVSSADKCE 168

RESULT 14

D36858
gene GAR protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Fro
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46888
A:Accession: S46888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449
A:Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protectiv
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: GAR
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 6.0%; Score 206.5; DB 2; Length 349;
Best Local Similarity 34.1%; Pred. No. 2.9e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;

Qy 65 LTCDCPCAGTYVSEHCTNTSLRVSCSPVGTFTTRHENGIEKCHDCSPCPWPMIEKLPCA 124
Db 42 LCCLSCPPTGYASRLCDSKNTQCTPCGSGFTSRNNHLPACLSGRCNSNQVETRSCN 101
Qy 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGWVKRGKTETEDVRCKQCARGTFSD 178
Db 102 TTHNRICEPSFGYICLLKSGSCKACVSTQKCGIGYV-SGHTSVGDVICSFGFGTYSH 160
Qy 179 VPSSVMKCK 187
Db 161 TVSSADKCE 169

RESULT 15

A42086
CD30 antigen precursor - human
N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A42086
R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A:Title: Molecular cloning and expression of a new member of the nerve growth factor re
A:Reference number: A42086; MUID:92154659; PMID:1310894
A:Accession: A42086
A:Molecule type: mRNA
A:Residues: 1-595 <DUR>
A:Cross-references: GB:M83554; NID:G180095; PIDN:AAA51947.1; PID:G180096
A:Experimental source: HUT-102 cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
C:Genetics:
A:Gene: GDB:CD30; DIS166E
A:Cross-references: GDB:I31547; OMIM:153243
A:Map position: 1p36-1p36
C:Superfamily: NGF receptor repeat homology
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-383/Domain: extracellular #status predicted <EXT>
F:384-407/Domain: transmembrane #status predicted <TM>
F:408-595/Domain: intracellular #status predicted <CYT>
F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 205; DB 2; Length 595;
Best Local Similarity 20.2%; Pred. No. 7.1e-06;
Matches 13; Conservative 66; Mismatches 250; Indels 200; Gaps 24;
Qy 30 LLLILG--FLSTTTAQEQK--ASNLGTGYRH-VDRATGQVLTCDKCPAGTYVSEHCTNTS 84
Db 5 LAALGLLFGALRAFFQDRPFEDTCHGNPSHYDKAVRR--CCYRCPMGLFFPQQCPQRP 62
Qy 85 LRVCSGCPVGTFTTRHENGIEKCHDCSPCPWPMIEKLPCAALTDRECTCPGMPF----- 138
Db 63 TDCRQCEPPIYLDADRCTACTCGRD---DLVETPCAWNSRVRCECRPGMFCSTSAV 119

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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:38:22 ; Search time 33 Seconds
(without alignments)
1024.697 Million cell updates/sec

Title: US-10-663-157-2

Perfect score: 3456

Sequence: 1 MGTSPSSSTALASCSRIARR.....SOEASQTLLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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4: /cgn2_6/prodata/2/iaa/5B-COMB.pep:*
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6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3456	100.0	555	4	US-09-527-236A-2
2	3456	100.0	555	4	US-09-314-844F-2
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4	3450	99.8	655	3	US-08-959-382-2
5	2892	83.7	605	3	US-09-042-785A-23
6	2723	78.8	573	3	US-09-042-785A-2
7	1359	39.3	253	3	US-09-042-785A-4
8	841	24.3	147	4	US-09-527-236A-19
9	841	24.3	147	4	US-09-756-854-19
10	673	19.5	125	3	US-08-959-382-4
11	673	19.5	125	4	US-09-314-844F-4
12	548	15.9	102	4	US-09-314-844F-6
13	431	12.5	84	3	US-09-042-785A-30
14	431	12.5	84	3	US-09-042-785A-31
15	352	10.2	67	4	US-09-527-236A-21
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17	343.5	9.9	461	1	US-08-385-229-2
18	343.5	9.9	461	2	US-08-650-000-2
19	343.5	9.9	461	3	US-09-042-785A-7
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21	343.5	9.9	461	3	US-09-006-353A-4
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23	343.5	9.9	461	4	US-09-573-986-4
24	343.5	9.9	461	4	US-08-406-824A-2
25	343.5	9.9	461	4	US-09-800-909-2
26	343.5	9.9	461	4	US-09-758-124-2
27	343.5	9.9	461	4	US-09-800-908-3

28 343.5 9.9 461 6 5395760-2 Patent No. 5395760
29 312.5 9.0 518 1 US-08-385-229-4 Sequence 4, Appli
30 312.5 9.0 518 4 US-09-579-845-1 Sequence 1, Appli
31 312.5 9.0 518 4 US-09-579-845-3 Sequence 3, Appli
32 366.5 8.9 235 4 US-09-326-394-4 Sequence 2, Appli
33 366.5 8.9 235 4 US-09-580-235-2 Sequence 2, Appli
34 366.5 8.9 235 4 US-09-580-235-8 Sequence 8, Appli
35 366.5 8.9 235 4 US-09-580-181-2 Sequence 2, Appli
36 366.5 8.9 235 4 US-09-580-181-8 Sequence 8, Appli
37 366.5 8.9 235 4 US-09-102-530-2 Sequence 2, Appli
38 366.5 8.9 235 4 US-09-102-530-8 Sequence 8, Appli
39 366.5 8.9 257 4 US-09-579-845-10 Sequence 10, Appli
40 305.5 8.8 235 4 US-09-580-235-4 Sequence 4, Appli
41 305.5 8.8 235 4 US-09-580-235-6 Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-527-236A-2
; Sequence 2, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-2

Query Match 100.0%; Score 3456; DB 4; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.6e-299;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSPSSSTALASCSRIARRATMTAGSLLLGLFLSTTTAQPEQKASNLIGYRHVDRA 60
Db 1 MGTSPSSSTALASCSRIARRATMTAGSLLLGLFLSTTTAQPEQKASNLIGYRHVDRA 60
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Db 121 LPCAALTDRECTCPGMFQSNATCAPHTVCPGVGVRKKGTETEDYRCKOCARGTSDVP 180
Qy 181 SSVMKCXYTDCLSQNLVTKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPEHMETHE 240
Db 181 SSVMKCXYTDCLSQNLVTKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPEHMETHE 240
Qy 241 VPSSTYVPKGMNSTESNSASVRPKVLSSIQEGTVFDNTSSARGKEDVNTKLTNLQVNH 300

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Db      241  VPSSTVVPKGMNSTESNSASVRPKVLSSIQBGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
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Db      301  QCGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHGFIDINEHLPMWIVLFLLL 360
QY      361  VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWIYYCNGHGIDILK 420
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QY      421  LVAAQVGSQWKDIYQFLCNASEREVAAPFNGYTAHERAYAAALQHWITIRGPASLAQLIS 480
Db      421  LVAAQVGSQWKDIYQFLCNASEREVAAPFNGYTAHERAYAAALQHWITIRGPASLAQLIS 480
QY      481  ALRQHRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
Db      481  ALRQHRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
QY      541  SPQDKNGKGFVDESEPLELRCDSSTSSGSSALSNGSFITKEKXDTVLRQVRLDPCDLQPIF 600
Db      541  SPQDKNGKGFVDESEPLELRCDSSTSSGSSALSNGSFITKEKXDTVLRQVRLDPCDLQPIF 600
QY      601  DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
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RESULT 2

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US-09-314-844F-2
; Sequence 2, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-314-844F-2

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Best Local Similarity 100.0%; Pred. No. 2.6e-299;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAQEQKASNLIGTYRHVDRA 60
Db      1  MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAQEQKASNLIGTYRHVDRA 60
QY      61  TGOVLTCDCPKAGTYVSEHCTNTSLRVSCSCVPVGTFRHENGIEKCHDCSQCPWPMEIK 120
Db      61  TGOVLTCDCPKAGTYVSEHCTNTSLRVSCSCVPVGTFRHENGIEKCHDCSQCPWPMEIK 120
QY      121  LPCAALTIRECTCPGPMFOSNATCAPHTVCPVGWVRKXGTETEDVRCKQARGTFSVDP 180
Db      121  LPCAALTIRECTCPGPMFOSNATCAPHTVCPVGWVRKXGTETEDVRCKQARGTFSVDP 180
QY      181  SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPSFSSSTSPSPGTAIFRPPHEMETH 240
Db      181  SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPSFSSSTSPSPGTAIFRPPHEMETH 240

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QY      241  VPSSTVVPKGMNSTESNSASVRPKVLSSIQBGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
Db      241  VPSSTVVPKGMNSTESNSASVRPKVLSSIQBGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
QY      301  QCGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHGFIDINEHLPMWIVLFLLL 360
Db      301  QCGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHGFIDINEHLPMWIVLFLLL 360
QY      361  VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWIYYCNGHGIDILK 420
Db      361  VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWIYYCNGHGIDILK 420
QY      421  LVAAQVGSQWKDIYQFLCNASEREVAAPFNGYTAHERAYAAALQHWITIRGPASLAQLIS 480
Db      421  LVAAQVGSQWKDIYQFLCNASEREVAAPFNGYTAHERAYAAALQHWITIRGPASLAQLIS 480
QY      481  ALRQHRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
Db      481  ALRQHRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
QY      541  SPQDKNGKGFVDESEPLELRCDSSTSSGSSALSNGSFITKEKXDTVLRQVRLDPCDLQPIF 600
Db      541  SPQDKNGKGFVDESEPLELRCDSSTSSGSSALSNGSFITKEKXDTVLRQVRLDPCDLQPIF 600
QY      601  DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
Db      601  DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655

```

RESULT 3

```

US-09-756-854-2
; Sequence 2, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
;               Yu, Guo-Liang
;               Fan, Ping
;               Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-756-854-2
Query Match      100.0%; Score 3456; DB 4; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.6e-299;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSLTTTAQPEQKASNLIGTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSLTTTAQPEQKASNLIGTYRHVDRA 60
QY 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120
DB 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120
QY 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTETEDVRCKQARGTFSDVP 180
DB 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTETEDVRCKQARGTFSDVP 180
QY 181 SSVMKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
QY 241 VPSSTVYVPGKMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYKTLPLNQVYVNH 300
DB 241 VPSSTVYVPGKMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYKTLPLNQVYVNH 300
QY 301 QQGFPHRHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMI VLFLL 360
DB 301 QQGFPHRHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMI VLFLL 360
QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYNCGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYNCGHGIDILK 420
QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGVTADHERAYAAALQHWITIRGEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGVTADHERAYAAALQHWITIRGEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPISPSPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPISPSPNAKLENSALLTVEP 540
QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKTIVLRQVRLDPCDLOPIF 600
DB 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKTIVLRQVRLDPCDLOPIF 600
QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLTLDVSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLTLDVSVYSHLPDLL 655

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RESULT 4

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US-08-959-382-2
; Sequence 2, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR7
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAINER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-959-382-2

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Query Match      99.8%; Score 3450; DB 3; Length 655;
Best Local Similarity 99.8%; Pred. No. 8.8e-299;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSLTTTAQPEQKASNLIGTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSLTTTAQPEQKASNLIGTYRHVDRA 60
QY 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120
DB 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120
QY 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTETEDVRCKQARGTFSDVP 180
DB 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTETEDVRCKQARGTFSDVP 180
QY 181 SSVMKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
QY 241 VPSSTVYVPGKMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYKTLPLNQVYVNH 300
DB 241 VPSSTVYVPGKMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYKTLPLNQVYVNH 300
QY 301 QQGFPHRHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMI VLFLL 360
DB 301 QQGFPHRHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMI VLFLL 360
QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYNCGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYNCGHGIDILK 420
QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGVTADHERAYAAALQHWITIRGEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGVTADHERAYAAALQHWITIRGEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPISPSPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPISPSPNAKLENSALLTVEP 540
QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKTIVLRQVRLDPCDLOPIF 600
DB 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKTIVLRQVRLDPCDLOPIF 600
QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLTLDVSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLTLDVSVYSHLPDLL 655

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Db 122 TKETDNUVCGMLFFSSTNPPSSGTVTFSPHEMESHDVPSSTYEPQGMNSTDNSASTASVR 181
Qy 264 PKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNVHCOGPHHRLKLLP-SNEATGGE 322
Db 182 TKVPEGIEEGTVPDNTSSARGKEDVNTKLPNLQVNVHCOGPHHRLKLLPSSWEAT-GE 240
Qy 323 KSSTPIKPGKRGHPQNLKHFIDINEHLPNMVILFLLVLVIVVCSIRKSSRTLKKGPR 382
Db 241 KSSTAIAKAPKRGHPQNAKHFIDINEHLPNMVILFLLVLVIVVCSIRKSSRTLKKGPR 300
Qy 393 QDPSAIVKAGIKKSMSTQNRKWIYYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASE 442
Db 301 QDPSAIVKAGIKKSLTTPQNRKWIYYRNGHGIDILKLVAAQVGSQWKDIYQFLCNASE 360
Qy 443 REVAAFSGYTAADHERAVALQHWITIRGPASLAQLISALRQHRRNDVVEKIRGLMEDTT 502
Db 361 REVAAFSGYTAADHERAVALQHWITIRGPASLAQLISALRQHRRNDVVEKIRGLMEDTT 420
Qy 503 QLETDKALPMSPLSPSPSPNAKLENSALLTVBPSPQDKNGKFFVDESEPLRCDS 562
Db 421 QLETDKALPMSPLSPSPSPFNKLENSALLTVBPSPQDKNGKFFVDESEPLRCDS 480
Qy 563 TSSGSSALSRGSGFTTKKKTDLQVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAE 622
Db 481 TSSGSSALSRGSGFTTKKKTDLQVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAE 540
Qy 623 DKLDLRFIIIGVKSQEAASQTLDSVYSHLPDLL 655
Db 541 DKLDLRFIIIGVKSQEAASQTLDSVYSHLPDLL 573

RESULT 7

US-09-042-785A-4
; Sequence 4, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-042-785A-4

Query Match 39.3%; Score 1359; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.9e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSPSSSTALASCSPRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCSPRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
Qy 61 TGOVLTCDCPCAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPMEIK 120
Db 61 TGOVLTCDCPCAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPMEIK 120
Qy 121 LPCAALTDRECTCPPGMFOSNATCAPHTVCPVGMGVRKGTETEDVRCKQCARGTSDVP 180
Db 121 LPCAALTDRECTCPPGMFOSNATCAPHTVCPVGMGVRKGTETEDVRCKQCARGTSDVP 180
Qy 181 SSVNWKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPCTAIFPRPEHMETHE 240
Db 181 SSVNWKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPCTAIFPRPEHMETHE 240
Qy 241 VPSSTYVVPK 249
Db 241 VPSSTYVVPK 249

RESULT 8

US-09-527-236A-19
; Sequence 19, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-19

Query Match 24.3%; Score 841; DB 4; Length 147;
Best Local Similarity 99.3%; Pred. No. 3.9e-67;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 66 TCDKCPAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPMEIKLPCAA 125
Db 1 TCDKCPAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPMEIKLPCAA 60
Qy 126 LTDRECTCPPGMFOSNATCAPHTVCPVGMGVRKGTETEDVRCKQCARGTSDVPSSVMK 185
Db 61 LTDRECTCPPGMFOSNATCAPHTVCPVGMGVRKGTETEDVRCKQCARGTSDVPSSVMK 120
Qy 186 CKAYTDCLSQNLVVIKPGTKETDNVCG 212
Db 121 CKAYTDCLSQNLVVIKPGTKETDNVCG 147

RESULT 9

US-09-756-854-19


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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 125
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-314-844F-4

Query Match
Best Local Similarity 19.5%; Score 673; DB 4; Length 125;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATWAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA 60
DB 1 MGTSPSSSTALASCSRIARRATATWAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA 60

QY 61 TQVLTCDKCPAGTVVSHCHTNTSLRVCSGPCVGTFTTRHENGIEKCHDCSQPCWPMTIEK 120
DB 61 TQVLTCDKCPAGTVVSHCHTNTSLRVCSGPCVGTFTTRHENGIEKCHDCSQPCWPMTIEK 120

QY 121 LPCAA 125
DB 121 LPCAA 125

RESULT 12
US-09-314-844F-6
; Sequence 6, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: RECEPTOR TR7
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-314-844F-6

Query Match
Best Local Similarity 15.9%; Score 548; DB 4; Length 102;
Matches 98; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA TQVLTCDKCPAGTVVSHCHTNTS 84
DB 1 MIAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA TQVLTCDKCPAGTVVSHCHTNTS 60

QY 85 LRVCSGPCVGTFTTRHENGIEKCHDCSQPCWPMTIEKLPCAA 125
DB 61 LRVCSGPCVGTFTTRHENGIEKCHDCSQPCWPMTIEKLPCAS 101

RESULT 13
US-09-042-785A-30
; Sequence 30, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-30

Query Match
Best Local Similarity 12.5%; Score 431; DB 3; Length 84;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAALQHWITIRGPEAS 474
DB 1 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAALQHWITIRGPEAS 60

QY 475 LAQLISALRQHRNDVVEKIRGLM 498
DB 61 LAQLISALRQHRNDVVEKIRGLM 84

RESULT 14
US-09-042-785A-31
; Sequence 31, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
```



```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-042-785A-31

Query Match 12.5%; Score 431; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GIDILKLVAAQVGSQWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEAS 474
Db 1 GIDILKLVAAQVGSQWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEAS 60

QY 475 LAQLISALRQHRNDVVEKIRGLM 498
Db 61 LAQLISALRQHRNDVVEKIRGLM 84

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RESULT 15
US-09-527-236A-21
; Sequence 21, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-527-236A-21

Query Match 10.2%; Score 352; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 QWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEASLAQLISALRQHRN 488
Db 1 QWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEASLAQLISALRQHRN 60

QY 489 DVVEKIR 495
Db 61 DVVEKIR 67

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:34:42 ; Search time 25 seconds
(without alignments)
1364.238 Million cell updates/sec

Title: US-10-663-157-2
Perfect score: 3456
Sequence: 1 NGTSPSSTALASCSRIARR.....SQEASQTLDSVSHLPDLL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
/ Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3456	100.0	655	1 TR21_HUMAN	Q9509 homo sapien
2	3059	88.5	655	1 TR21_MOUSE	Q9509 mus musculu
3	343.5	9.9	461	1 TR1B_HUMAN	P20333 homo sapien
4	304.5	8.8	401	1 TR1B_RAT	O08727 rattus norv
5	301.5	8.7	401	1 TR1B_HUMAN	O00300 homo sapien
6	301.5	8.7	401	1 TR1B_MOUSE	O08712 mus musculu
7	287	8.3	300	1 TR6B_HUMAN	O95407 homo sapien
8	273.5	7.9	474	1 TR1B_MOUSE	P25119 mus musculu
9	238	6.9	415	1 TRR3_MOUSE	P50284 mus musculu
10	236.5	6.8	416	1 TR16_CHICK	P18519 gallus gall
11	235.5	6.8	255	1 TRR9_HUMAN	Q07011 homo sapien
12	233	6.7	289	1 TRR5_MOUSE	P27512 mus musculu
13	228.5	6.6	435	1 TRR3_HUMAN	P36941 homo sapien
14	227	6.6	269	1 TRR5_BOVIN	Q28203 bos taurus
15	218.5	6.3	326	1 VTR2_MXVL	P29825 myxoma viru
16	215.5	6.2	351	1 CRMB_COWPX	O73559 cowpox viru
17	211.5	6.1	325	1 VTR2_SPVKA	P05943 Shope fibro
18	211.5	6.1	425	1 TR16_RAT	P07174 rattus norv
19	210.5	6.1	427	1 TR16_HUMAN	P08138 homo sapien
20	208.5	6.0	349	1 CRMB_CAMPS	Q9uy47 camelipox vi
21	206.5	6.0	349	1 CRMB_VARV	P34015 variola vir
22	206	6.0	625	1 TR11_MOUSE	O35305 mus musculu
23	205.5	5.9	616	1 TR11_HUMAN	Q9y6g6 homo sapien
24	205	5.9	283	1 TR14_HUMAN	Q2956 homo sapien
25	205	5.9	595	1 TRR8_HUMAN	P28908 homo sapien
26	200	5.8	277	1 TRR5_HUMAN	P25942 homo sapien
27	199.5	5.8	417	1 TR16_MOUSE	Q920w1 mus musculu
28	195	5.6	471	1 TR1A_BOVIN	O19131 bos taurus
29	193	5.6	461	1 TR1A_PIG	P50555 sus scrofa
30	187.5	5.4	493	1 TRR8_RAT	P97525 rattus norv
31	186.5	5.4	461	1 TR1A_RAT	P22934 rattus norv
32	180.5	5.2	256	1 TRR9_MOUSE	P20334 mus musculu
33	176	5.1	498	1 TRR8_MOUSE	Q50846 mus musculu

34	175	5.1	176	1	TR23_MOUSE	Q9et63 mus musculu
35	170	4.9	454	1	TR1A_MOUSE	P25118 mus musculu
36	162	4.7	259	1	TR10C_HUMAN	O14798 h tumor nec
37	154	4.5	277	1	TRR4_HUMAN	P43489 homo sapien
38	149.5	4.3	1193	1	TRR2_HUMAN	Q13753 homo sapien
39	148	4.3	271	1	TRR4_RAT	P15725 rattus norv
40	146	4.2	198	1	TR22_MOUSE	Q9et62 mus musculu
41	145.5	4.2	455	1	TR1A_HUMAN	P19438 homo sapien
42	143	4.1	204	1	TR26_MOUSE	P83626 mus musculu
43	142	4.1	417	1	TR25_HUMAN	Q93038 h tumor nec
44	136	3.9	272	1	TRR4_MOUSE	P47741 mus musculu
45	135.5	3.9	5376	1	ZAN_MOUSE	O88799 mus musculu

ALIGNMENTS

RESULT 1
TR21_HUMAN
ID TR21_HUMAN STANDARD; PRT; 655 AA.
AC Q75509; Q96D86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE tumor necrosis factor receptor superfamily member 21 precursor (TNFR- related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98378343; PubMed=9714541;
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";
RT FEBS Lett. 431:351-356 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Colon;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heitort E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinaki M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -/- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -/- SUBUNIT: Associates with TRADD.
CC -/- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -/- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalus D.B., Schnercher A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4].

FUNCTION

RX MEDLINE=21571606; PubMed=11714751;

RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.; "Impaired c-Jun amino terminal kinase activity and T cell differentiation in death receptor 6-deficient mice.";

RL J. Exp. Med. 194:1441-1448 (2001).

CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By similarity). May activate JNK and be involved in T-cell differentiation.

CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis. May be involved in T-cell differentiation.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen, thymus, testis, prostate, ovary, small intestine, colon, brain, lung and kidney, and in fetal brain, liver and lung. Detected at lower levels in adult peripheral blood leukocytes, lung, and in fetal muscle, heart, kidney, small intestine and skin. Detected in T-cells, B-cells, and monocytes. In T-cells expression is highest in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.

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DR EMBL; AF322069; AAC38115.1; -

DR EMBL; AY043489; AAK74193.1; -

DR EMBL; BC016420; AAH16420.1; -

DR HSP; O14763; 1D0G.

DR MGD; MGI:2151075; Tnfrsf21.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 1.

KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 41

FT CHAIN 42 655

FT TUMOR NECROSIS FACTOR RECEPTOR

FT SUPERFAMILY MEMBER 21.

FT DOMAIN 42 349

FT TRANSMEM 350 370

FT POTENTIAL.

FT DOMAIN 371 655

FT CYTOPLASMIC (POTENTIAL).

FT DEATH.

FT REPEAT 50 88

FT TNFR-CYS 1.

FT REPEAT 90 131

FT TNFR-CYS 2.

FT REPEAT 133 167

FT TNFR-CYS 3.

FT REPEAT 170 211

FT TNFR-CYS 4.

FT BY SIMILARITY.

FT DISULFID 67 80

FT DISULFID 70 88 BY SIMILARITY.

FT DISULFID 91 106 BY SIMILARITY.

FT DISULFID 109 123 BY SIMILARITY.

FT DISULFID 113 131 BY SIMILARITY.

FT DISULFID 133 144 BY SIMILARITY.

FT DISULFID 150 168 BY SIMILARITY.

FT DISULFID 171 186 BY SIMILARITY.

FT DISULFID 192 211 BY SIMILARITY.

FT CARBOHYD 82 92 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 257 257 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 352 352 W -> L (IN REF. 1).

FT CONFLICT 523 523 M -> I (IN REF. 3).

SQ SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99BEFF7 CRC64;

Query Match 88.5%; Score 3059; DB 1; Length 655;

Best Local Similarity 88.9%; Pred. No. 3,7e-193;

Matches 593; Conservative 19; Mismatches 52; Indels 2; Gaps 2;

QY 1 MGTSPSSSTALASCRIARRATATMTAGSLLLGLSTTTAQPEOKASNLICTYRHVDRA 60

DB 1 MGTSSITLALASCSTAGQVATWAGSLLLGLSTTTAQPEOKTUSLPGTYRHVDRT 60

QY 61 TGOVLTCDCPCAGTYVSEHCTNLSRVSCSCPVGTFTRHENGIEKCHDCSQCPWPMIEK 120

DB 61 TGOVLTCDCPCAGTYVSEHCTNLSRVSCSCPAGTFTRHENGIERCHDCSQCPWPMIEK 120

QY 121 LPCAALTDRETCPPGPMFOSNATCAPHTVCPVGVGVRKKGTTEDVRCQCARGFSDVP 180

DB 121 LPCAALTDRETCPPGPMYQSNATCAPHTVCPVGVGVRKKGTTEDVRCQCARGFSDVP 180

QY 181 SSMKCKAYTDCLSQNLVVKGTETDNVCGTLPSFSSSTSPSGTALFPPPEHMETHE 240

DB 181 SSMKCKAHIDCLQWLEVKGTETDNVCGNR.LFSSSTNPSSGTVTFSPPEHMETHE 240

QY 241 VPSSTVYVPGMNSTESNASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300

DB 241 VPSSTVYVPGMNSTDSNSTASVRTKVPSCIEEGTVPDNTSSARGKEDVNKTLPLNQVNH 300

QY 301 QQCPHRRHILKLP-SMEATGEGKSTPIKGRKGRHPRONLKHFDINEHLPMVILFLL 359

DB 301 QQCPHRRHILKLP-SMEAT-GEKSSATLAKPRGRHPRONLKHFDINEHLPMVILFLL 359

QY 360 LVLVIVVCSIRKSSRTLKKGPRQPSAIVEXAGLKKSMPTQNREKWIYCNHGIDIL 419

DB 360 LVLVIVVCSIRKSSRTLKKGPRQPSAIVEXAGLKKSLTPQNREKWIYCNHGIDIL 419

QY 420 KLVAAGVGSQWKDIYQFLCNASEREVAAPFNSGYTADHERAYAAALQHWITIRGEASLAQL 479

DB 420 KLVAAGVGSQWKDIYQFLCNASEREVAAPFNSGYTADHERAYAAALQHWITIRGEASLAQL 479

QY 480 SALRQHRNDVVEKIRGLMEDTQLETDKLALPMSPSPSPSPSPSPSPSPSPSPSPSPSPSP 539

DB 480 SALRQHRNDVVEKIRGLMEDTQLETDKLALPMSPSPSPSPSPSPSPSPSPSPSPSPSPSP 539

QY 540 PPSQDKNKGFFVDESEPLLRCDSTSGSSSALSRNGSFFITKEKDTVLROVRLDPCDLQPI 599

DB 540 PPSLDKNKCFVDESEPLLRCDSTSGSSSALSRNGSFFITKEKDTVLROVRLDPCDLQPI 599

QY 600 FDDMLHFTNPEELRVIEETPOAEDKDLRLFEILGVKSOEASQTLTLDVSVSHLPDLL 655

DB 600 FDDMLHFTNPEELRVIEETPOAEDKDLRLFEILGVKSOEASQTLTLDVSVSHLPDLL 655

RESULT 3

TRIB HUMAN STANDARD; PRT; 461 AA.

ID TRIB_HUMAN

AC P20333; Q16042; Q9UHL1;

DT 01-FEB-1991 (Rel. 17, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p75) (TNFR-R2) (ETARcept)
DE [Contains: Tumor necrosis factor binding protein 2 (TNFR2)]
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90260639; PubMed=2160731;
RX Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RN SEQUENCE FROM N.A., AND VARIANT ARG-196.
RP MEDLINE=91045991; PubMed=2172983;
RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=96299745; PubMed=8661109;
RX Belinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RN SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
RP ARG-301.
RX Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP TISSUEPNS;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Perge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Vax S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
RN [7]
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [8]
RN SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=1117652;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
RN [9]
RN SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [10]
RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [11]
RN CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [12]
RN INTERACTION WITH TRAF2.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
RN [14]
RN VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21633888; PubMed=11762942;
RA Morita C., Horiuchi T., Tsukamoto H., Hatta N., Kikuchi Y.,
RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;
RT "Association of tumor necrosis factor receptor type II polymorphism
RT 196R with systemic lupus erythematosus in the Japanese: molecular and
RT functional analysis.";
RL Arthritis Rheum. 44:2819-2827(2001).
RN [15]
RN VARIANT ARG-196.
RX MEDLINE=22151311; PubMed=12161545;
RA Peral B., San Millan J.L., Castello R., Moghetti P.,
RA Escobar-Morreale H.F.;
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic
RT ovary syndrome and hyperandrogenism.";
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).
CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and

approximately 5-fold lower affinity for homotrimeric TNF α /lymphotoxin- α . The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF receptor 2 mediates most of the metabolic effects of TNF- α .

-1- SUBUNIT: Binds to TRAF2.

-1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.

-1- PM: Phosphorylated; mainly on serine residues and with a very low level on threonine residues.

-1- PM: A soluble form (tumor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing.

-1- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consists of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin FC chain. It binds to TNF- α and blocks its interactions with receptors.

-1- SIMILARITY: Contains 4 TNFR-Cys repeats.

-1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
WWW='http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm'.

-1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
WWW='http://www.enbrel.com/'.

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EMBL; M32315; AAC59929.1; --
DR EMBL; U52165; AAC50622.1; --
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; --
DR EMBL; AY264804; AAC89076.1; --
DR EMBL; AY342040; AAP88939.1; --
DR EMBL; BC052977; AAH52977.1; --
DR EMBL; S63368; BAB19824.2; --
DR EMBL; M35858; AAA63262.1; --
DR EMBL; AB030950; BAA89053.1; --
DR PIR; A35356; A35356.
DR Genew; HGNC:11917; TNFRSF1B.
DR

```

Query Match          9.9%; Score 343.5; DB 1; Length 461;
Best Local Similarity 29.2%; Pred. No. 2.6e-15;
Matches 95; Conservative 35; Mismatches 116; Indels 79; Gaps 11;

QY      65 LTCDKCPAGTYVSEHCTNTSLRYCSSCPVGTFIRPHENGIEKCHDCSPCCWPMIEKLPCA 124
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      52 MCCSKCSPGOAHKVCFKTSIDTVCDSCEDSTYTQLMNWPECLSGSRCSDDQVETQACT 111

QY     125 ALTDRECTCPGMPF-----QSNATCAPHTVCPVGMGRKKGTETEDEVRCQCARGTFSFD 178
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     112 REQNRICTRPGWCALSKOEGCFLCAPLKRCPGFVARPGETSDVCVKPCAPGTFSN 171

QY     179 VPSSVMCKAYTDCLSNLNVIKPTKETDNVCGTGLPSFSSSTSP-----SPGTAIPRRP-- 233
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     172 TTSSTDICRPHQIC---NWVAI-PGNASMDAVC-----TSTSPTSMAPGAVHLPPV 220

QY     234 ----EHMETHEVPVS----STYPVKGMKSTESNSS-----259
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     221 STRSOHQTPPETPTAESTFLLPMGPSPPAEGSGDFAIPVLGVLTGALLIGVN 280

QY     260 ----ASYRPKVLSSIQBGTVPD-NTSSARGKEDVNKTLPLQVVNHOQQGPHRHILKLP 314
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 261 CVINTQVKKKPLCLQREAKVPHLPADKARG-----TQSPQQHLITAP 324

Qy 315 SMEATGCKSKSTPI--KGPKRGHPH 337
|::||:::||:

Db 325 SSSSSLESSASALDREAPTNPQ 349

RESULT 4

T11B_RAT	ID	T11B_RAT	STANDARD;	PRT;	401 AA..				
AC	O05727;								
DT	28-FEB-2003	(Rel. 41, Created)							
DT	28-FEB-2003	(Rel. 41, Last sequence update)							
DE	28-FEB-2003	(Rel. 41, Last annotation update)							
DE	Tumor necrosis factor receptor superfamily member 11b precursor								
DE	(Osteoprotegerin).								
GN	TNFRSF11B OR OPG.								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
OX	NCB1_TaxID=10116;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Embryonic intestine;								
RC	MEDLINE=97262071; PubMed=9108485;								
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,								
RA	Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,								
RA	Derosé M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,								
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,								
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,								
RA	Suggs S., Boyle W.J.;								
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation								
RT	of bone density."								
RL	Cell 89:309-319(1997).								
CC	-!	FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis (by similarity).							
CC	-!	SUBUNIT: Homodimer (By similarity).							
CC	-!	SUBCELLULAR LOCATION: Secreted (By similarity).							
CC	-!	INDUCTION: Upregulated by osteopontin.							
CC	-!	SIMILARITY: Contains 4 TNFR-Cys repeats.							
CC	-!	SIMILARITY: Contains 2 death domains.							
CC	-----								
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CC	-----								
DR	EMBL;	U94330;	AAB53707.1;	--					
DR	HSSP;	P25942;	1CDF.						
DR	InterPro;	IPR000488;	Death.						
DR	InterPro;	IPR001368;	TNFR_C6.						
DR	Pfam;	PF00020;	TNFR_C6; 4.						
DR	SMART;	SMC0005;	DEATH; 1.						
DR	SMART;	SMC0208;	TNFR; 4.						
DR	PROSITE;	PS50017;	DEATH_DOMAIN; FALSE_NEG.						
DR	PROSITE;	PS00652;	TNFR_NGRF_1;	1.					
DR	PROSITE;	PS50050;	TNFR_NGRF_2;	2.					
KW	Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.								
FT	SIGNAL	1	21	BY SIMILARITY.					
FT	CHAIN	22	401	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.					
FT	REPEAT	24	62	TNFR-CYS 1.					
FT	REPEAT	65	105	TNFR-CYS 2.					
FT	REPEAT	107	142	TNFR-CYS 3.					
FT	REPEAT	145	185	TNFR-CYS 4.					

FT DOMAIN 198 269 DEATH 1.
 FT SITE 270 365 DEATH 2.
 FT DISULFID 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 401 AA; 46192 MW; FFC6A31FD4E573A CRC64;
 Query Match 8.8%; Score 304.5; DB 1; Length 401;
 Best Local Similarity 28.6%; Pred. No. 7.8e-13;
 Matches 91; Conservative 44; Mismatches 142; Indels 41; Gaps 9;

QY 30 LLLGLFLSTTAQ--PEQKASNLIGTYRHVDRTGQVLTCDKPCAGTVVSHCTNTSLRV 87
 DB 10 LVFLDIETWTQETPPK-----YLHYDETGRQLLCKDCAPGYLYKGCHCIVRKTL 61
 QY 88 CSSCPVGTFTRHENGIEKCHDCSPCPWPMIEKLPFCAALTDRECTCPGPMFQSNATCAPH 147
 DB 62 CVCPCDYSYDTSWHTSDECVYCSPVCKELQVQECNTRHVRCECEBGRYLEFCLXK 121
 QY 148 TVCPGWGVKKGTEDEVRCQCARGTFSVPSSVMKCKAYTCLSNLVVIFPGTKET 207
 DB 122 RSCPPGLQVLQAGTPEFTNVCKRCPDGFSGTSSKAPCRKHTNCSSGLGLLIQGNATH 181
 QY 208 DNVCGTLPSFSSTSPSPCTAIFPRPEHMETHEVPSSTYVPKGN-----STESNSA 260
 DB 182 DNVG-----SGNREATQNGIDVTLCEEAFFRAFPVTK-IIPNWLVLVDSLPGRKVAES 236
 QY 261 SVRPKVLASIQGTVP-----DWTSSARGKEDVNTKLPNLVQNVQOQPHHHI----- 309
 DB 237 VERIKRRHSSQETQLLKLWKHQN----RDQXVKKIIOIDLCSSVQRHGHANLTT 292
 QY 310 --LKLPSWEATGGRKSS 325
 DB 293 EQRLIL--MESLPGRKIS 308

RESULT 5

ID T11B HUMAN STANDARD; PRT; 401 AA.
 AC O00300; O60236; Q9UHP4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPB OR OCIF.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.O., Woodson B., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Sugis S., Boyle W.J.,
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";

RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung cancer;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Placenta;
 RX MEDLINE=98351569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Eve;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 22-36 AND 378-401.
 RX MEDLINE=98238645; PubMed=9571159;
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
 RA Morinaga T., Tsuda E., Higashio K.;
 RT "Characterization of monomeric and homodimeric forms of
 RT osteoclastogenesis inhibitory factor.";
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
 RN [6]
 RP SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 RN [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.;
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 RN [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Emery J.G., McDonnell P., Eichman C., DiPrinzio R., Dadds R.A.,
 RA Dul E., Appelbaum E.R., Eichen C., Young P.R.;
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RL J. Biol. Chem. 273:14363-14367(1998).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
 RT Morinaga T., Higashio K.;
 RT "Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hobbauer L.C., Neubauer A., Heufelder A.E.;
 RT "Receptor activator of nuclear factor-kappa ligand and
 RT osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC Detected at very low levels in brain, placenta and skeletal
 CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -!- INDUCTION: Upregulated by increasing calcium-concentration in the
 CC medium and estrogens. Downregulated by glucocorticoids.
 CC -!- PTM: N-glycosylated. Contains sialic acid residues.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 2 death domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U94332; AAB53709.1; -;
 DR EMBL; AB002146; BAA25910.1; -;
 DR EMBL; AB008822; BAA32076.1; -;
 DR EMBL; AB008821; BAA32076.1; JOINED.
 DR EMBL; BC030155; AAH30155.1; -;
 DR EMBL; AF134187; AAF20168.1; -;
 DR HSP; P25942; ICDP; -;
 DR Gene; HGNC:11909; TNFRSF11B.
 DR MIM; 602643; -;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007165; F:signal transduction; TAS.
 DR GO; GO:0001501; F:skeletal development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3-
 DR SMART; SM00005; TNFR; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT REPEAT 24 62
 FT TNFR-CYS 1.

FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT DOMAIN 270 365
 FT SITE 400 400
 FT SITE 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 107 118
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 98 98
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 3 3
 FT MUTAGEN 400 400
 FT MUTAGEN 400 401
 FT CONFLICT 263 263
 FT SEQUENCE 401 AA; 48040 MW; EDF448B67D86C71E CRC64;
 Query Match 8.7%; Score 301.5; DB 1; Length 401;
 Best Local Similarity 24.8%; Pred. No. 1.2e-12;
 Matches 102; Conservative 58; Mismatches 177; Indels 75; Gaps 13;
 SQ SEQUENCE 401 AA; 48040 MW; EDF448B67D86C71E CRC64;
 QY 54 YRHVDATQVLTCDKCPAGTVVSEHCTNTSLRVSCSPVGTFTRHENGIEKHCDSQPC 113
 DB 28 YLHDEETSHQLLDCDKCPGTLYLKHCTAKWTVCAPCDPHYTDSWHTSDECLYCSPVC 87
 QY 114 PWEVIEKLPAAALTDRECTCPFGFOSNATCATPTVCPVGMVGRKKGTEDEVRCQCAR 173
 DB 88 KELQYVQKQCNTHNRVCEKSGRYLEIEFCLKHSRCPFGVGVQAGTPTNVTVCRCPD 147
 QY 174 GTFSDVPSSVMKCAVTDCLSNLVVKGTEKTVCTNLTFSFSSSTSPSGTALFPPR 233
 DB 148 GFFSNSTSKAPCRKTNCSVFGLLTQGNATHDNIC-----SGNSESTKCGIDVTLC 203
 QY 234 EHMETHEVPSSTVPRKGMN-----STESNSASVRPKVLSIOEGTVP-----DNT 279
 DB 204 EAFPRAVPTK-FTFNWLSVLVDNLPSTKVAESVERIKRQSSQEQTQLKLWKHQN- 261
 QY 280 SSARGKEDVNTLPNLQVNVNHOOGPHRH-----ILKLLPSMEATGKESSTPIK 329
 DB 262 ---KDQDIVKKIQQIDLCENSQVRHIGHANLTFEQLRSLMESLPG-KKVGAEDIEKTIK 317
 QY 330 GPKRGHPRQNLKHGFDINEHLPKMWIVFLVLLVAVVWCVSIRKSSRTLKKGPRQDPSATV 389
 DB 318 ACK---PSDQILKLLSL-----WRI-----KNGQDQTLKGLM 346
 QY 390 EKAGLKKS-----MTPTQNRKWIYVNCNGHGIDIL--KLVAQVGSQWKDI 433
 DB 347 H--ALKHSKTYHPKTVTQSLKTRFLHSFTMYKLYQKLFLEMIGNQVQS 396
 RESULT 6
 T11B MOUSE
 ID T11B MOUSE STANDARD; PRT; 401 AA.
 AC O08712; O70202;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Kidney;
RC MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehly R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimanoto G.,
RA Davese M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [12]
RC SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RC AND ARG-296.
RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RC MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RN [3]
RC FUNCTION.
RC MEDLINE=21060987; PubMed=10952716;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT osteoclasts and prevents vascular calcification by blocking a process
RT resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-473(2000).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC intestines and calvaria. Highly expressed in decidua and placenta,
CC and in embryo.
CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC whereas expression decreases at day 11 and increases from day 15
CC to 17. On day 15 found in developing bone primordia,
CC brachiocephalic artery and ductus arteriosus, left main bronchus,
CC abdominal aorta and midgut.
CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U94331; AAB53708.1; -
CC EMBL; AB013898; BAA28269.1; -
CC EMBL; AB013903; BAA33388.1; -
CC EMBL; AB013899; BAA33388.1; JOINED.
CC EMBL; AB013900; BAA33388.1; JOINED.
CC EMBL; AB013901; BAA33388.1; JOINED.
CC EMBL; AB013902; BAA33388.1; JOINED.
CC HSSP; P25942; ICDF.
CC MGD; MGI:109587; Tnfrsf1b.

DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00552; TNFR_NGFR_1; 1.
DR PROSITE; PS00550; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT REPEAT 198 269
FT DOMAIN 283 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 138 138
FT VARIANT 161 161
FT VARIANT 165 165
FT VARIANT 288 288
FT VARIANT 296 296
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 1.2e-12;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;
QY 30 LLLLFSLTTTAQPEKASNLIGTVHRVDRATGQVLTCDKCPAGTYVSEHCNTSLRVCS 89
DB 10 LVLLDIIEITTOE-----TLPPKYLHYDPETGTHOLLCDKCAPGYLKHQHTVRKTKLV 63
QY 90 SCPVGTFTTHENGIEKCHDCSQPCPWPMEIKLPKCAALTDRECTPPGFMFQSNATCAPHTV 149
DB 64 PCPDHSYDTSWTSDECVYCSVCKELOSVKQECNTHNRVCECEGYLIEFCLKHRS 123
QY 150 CPVGVGVRKKGTETEDVCKQCARGTTFSDVSSVMKCKAYTDCLSQNLVWIKPGTKETDN 209
DB 124 CPPGSGVQAGTPERTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDN 183
QY 210 VCGTLPSPSSSTSPSGTAIFPRPHMETHVPFSSTVYPKGMN-----STENSSASV 262
DB 184 VC-----SGNREATQKGDIVLCEAFAFFRAVPTK-IIPNWLVLVDSLPGLKVAESVE 238
QY 263 RPKVLSSIQEGTVP-----DNTSARGKEDVNTKLPNLQVNHQCGPHRH-----ILK 311
DB 239 RIKRHSSEOQTQFOLLKLWQHON-----RDQEMVKIIQIDILCESSVQRHGHSLNLTTEQ 294
QY 312 LLPSVEATGGEKSS 325
DB 295 LLALMESLPGKKIS 308

RESULT 7
 TR56B_HUMAN STANDARD; PRT; 300 AA.
 AC O95407;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy)
 DE receptor for Fas ligand) (Decoy receptor 3) (Dcr3) (M68).
 GN TNFRSF6B OR DCR3 OR TR6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=fetal lung;
 RX MEDLINE=99087326; PubMed=9872321;
 RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Borstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer.";
 RL Nature 396:699-703(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RX MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RA "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 RL J. Biol. Chem. 274:13733-13736(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RA "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina X., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carroll P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahy J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 CC -!- SUBCELLULAR LOCATION: Secreted
 CC TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 CC Detected in adult stomach, spinal cord, lymph node, trachea,
 CC spleen, colon and lung. Highly expressed in several primary tumors
 CC from colon, stomach, rectum, esophagus and in SW480 colon
 CC carcinoma cells.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC -----
 CC EMBL; AF104419; AAD03056.1; -
 CC EMBL; AF134240; AAD29688.1; -
 CC EMBL; AF217796; AAF35244.1; -
 CC EMBL; AF217793; AAF33685.1; -
 CC EMBL; AF217794; AAF33686.1; -
 CC EMBL; AL121845; CAC03668.1; -
 CC EMBL; BC017065; AAL17065.1; -
 CC EMBL; BC034349; AAL34349.1; -
 CC HSP; O14763; IDOG.
 CC Genew; HGNC:11921; TNFRSF6B.
 CC MIM; 603361; -
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 CC GO; GO:0004872; F:receptor activity; TAS.
 CC GO; GO:0006916; P:anti-apoptosis; TAS.
 CC InterPro; IPR001368; TNFR_C6.
 CC Pfam; PFO020; TNFR_C6; 4.
 CC SMART; SMC0208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC PROSITE; PS50050; TNFR_NGFR_2; 2.
 CC Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 31 70 SUPERFAMILY MEMBER 6B.
 FT REPEAT 72 113 TNFR-CYS 1.
 FT REPEAT 115 150 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 193 229 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 95 113 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;
 Query Match 8.3%; Score 287; DB 1; Length 300;
 Best Local Similarity 34.3%; Pred. No. 7.5e-12;
 Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;
 QY 53 TYRVDVDRATGCVLTCDKPCAGTVVSEHCTNTSLRVCSQCVGTFTREHNGIEKCHDCSQP 112
 DB 35 TYFWRDAETGERLVCAQCPGTFVQPCRRDPTTCGPPPHRYTGFVWYLERCRYCNVL 94
 QY 113 CPNEMIEKLPFAALTDRCTCPGPMFSNATCAPIHTVCPVGMVRKKGTEDEVCKQCA 172
 DB 95 CGEREERARACHATHNRCRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQCP 154
 QY 173 RGTFSDFVPSVVMKRAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSST 221
 DB 155 PGTFSSASSSSSEOCQPHRNCTALGLALNVPGSSSHDTLCTCTGTGFLST 203

Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 Browning J.L., Ware C.F.;
 "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression.";
 J. Immunol. 155:5280-5288 (1995).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=96163885; PubMed=8586432;
 Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 Honjo T.;
 "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 sequence trap and chromosomal mapping.";
 Genomics 30:312-319 (1995).
 [3]
 INTERACTION WITH TRAF5.
 STRAIN=BALB/c;
 MEDLINE=96278943; PubMed=8663299;
 Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 Yagita H., Okumura K.;
 "TRAF5, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor";
 J. Biol. Chem. 271:14661-14664 (1996).
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTb, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs
 (By similarity).
 CC -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 CC
 CC EMBL; U29173; AAA68964.1; -.
 CC EMBL; L38423; AAB00846.1; -.
 CC EMBL; U30798; AAB81334.1; -.
 CC HSP; O14763; 1DOG.
 CC MGD; MGI:104875; Ltbr.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 3.
 CC SMART; SM00208; TNFR; 3.
 CC PROSITE; PS00652; TNFR_NGFR 1; 2.
 CC PROSITE; PS00500; TNFR_NGFR 2; 3.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 30
 FT CHAIN 31 415
 FT DOVAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 FT SEQUENCE 415 AA; 44956 MW; 29B326A56A6F61 CRC64;

Query Match 6.9%; Score 238; DB 1; Length 415;
 Best Local Similarity 23.5%; Pred No. 1.9e-08;
 Matches 95; Conservative 40; Mismatches 144; Indels 126; Gaps 17;
 QY 16 RIARRATATMIAGSLLIGLFTTTTAQPEQKASNIIGTYRHVDRAT-----GVV 64
 Db 2 RLPRASSPCGLAWGPLLGLSLVASQPQ-----LVPPYR-IENQTCWDQDKEYEYPMHD 56
 QY 65 LNCDCPKAGTYVSEHCTNTSLVCSQCPVGTTRFHENGIEKCHDCSQCPWPM--IEKLP 122
 Db 57 VCSRCPPGPEFVAVCSQDVTCKTCHNSNEHNLSTCLC-RPCDIVLGEVAP 115
 QY 123 CAALTDRECTCPGM---FQSN-----ATCAPHTVCPVGMVKKKGTE----- 164
 Db 116 CTSRKAECRCOPGMSCVYLDNECVHCEERLVLPQ-----GTEAEVTDIEI 162
 QY 165 ---DYRCKOCAGRTFSDVPSSVMKCKAYTDCLSQNLVLIKPGTKTDNVYCGTLPS----- 216
 Db 163 MTDVNCVPCXPGHFONTSSPRARCPHTRCISQGLVEAAPGTYSDTICKNPPBPBGAML 222
 QY 217 -----FSS-----STSPSPGTAIFRPEHEMTHETHEVPSSTYVPRGMNS 253
 Db 223 LLAILLSLVLLFTTTLACAMWRHPSLCRKLGLTLKRHPEGEESPPCPAPRADPH---- 278
 QY 254 TESNSASVRPKVLSSIQGTVP---DNTSSARGKEDVNKTLNPL-QVNVHQGP----- 304
 Db 279 -----FPDLAEPLPMSGDLSPSPAGP-----PTAPSLVEVYVLPQOQSLVQAR 321
 QY 305 -----HHRHLLKLLPSMEATGKESST-----PIKGPGRG 334
 Db 322 ELEAEPEGHQVANGANGHVTGGSVTVGNIIYNGFVLGSTRG 366
 RESULT 10
 TR16 CHICK
 ID TR16 CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp90-LNGFR)
 DE (p75 ICD) (low affinity neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90166579; PubMed=2560385;
 RA Large T.H., Weskamp G., Heider J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system.";
 RL Neuron 2:1123-1134 (1989).
 RN [2]
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE=90152140; PubMed=2154393;
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.";
 RL Dev. Biol. 137:287-304 (1990).
 CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC and NT-4. Can mediate cell survival as well as cell death of
 CC neural cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and TRAF3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: N- and O-glycosylated.

```

CC CC -!- PTM: Phosphorylated on serine residues.
CC CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC CC -!- SIMILARITY: Contains 1 death domain.
DR DR PIR; JN0006; JN0006.
DR DR HSP; P01714; INGR.
DR DR InterPro; IPR000488; Death.
DR DR InterPro; IPR001368; TNFR_c6.
DR DR Pfam; PF00531; Death; 1.
DR DR Pfam; PF00020; TNFR_c6; 4.
DR DR SMART; SM00005; DEATH; 1.
DR DR SMART; SM00208; TNFR; 3.
DR DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR DR PROSITE; PS00650; TNFR_NGFR_2; 3.
DR DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal.
FT SIGNAL 1 19
FT CHAIN 20 416
FT DOMAIN 29 239
FT TRANSMEM 240 261
FT DOMAIN 262 416
FT REPEAT 23 57
FT REPEAT 58 99
FT REPEAT 100 138
FT REPEAT 140 180
FT DOMAIN 333 410
FT DOMAIN 188 236
FT DISULFID 24 35
FT DISULFID 36 49
FT DISULFID 39 56
FT DISULFID 59 75
FT DISULFID 78 91
FT DISULFID 81 99
FT DISULFID 101 114
FT DISULFID 117 130
FT DISULFID 120 138
FT DISULFID 141 156
FT DISULFID 159 172
FT DISULFID 162 180
FT CARBOHYD 52 52
FT CONFLICT 36 36
FT CONFLICT 173 173
FT CONFLICT 276 276
FT CONFLICT 396 396
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;

Query Match
Best Local Similarity 6.8%; Score 236.5; DB 1; Length 416;
Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;
QY 67 CDKCPAGTYVSEHCTNTSLRYCSSC-PVGTETFRHENGIEKCHDCSQPCPWFMIKLPCAA 125
DB 36 KCACNLGEGVQPC-GVNGQTVCEPCLDSVTYSATEPCPKCTQ-CVGLHSMSPQVE 93
QY 126 LTRECTCPGFMQS--NATCAPTVGVGVGRKGTETEDVRCKOCARGTSDVPSSV 183
DB 94 SDDAVRCAYGYFODELGSCKECSICEVGFGLFPCRDQDVCCECPGEGTFSDEANFV 153
QY 184 MKCRAYTDCLQNLVWIKPGFKETDNVCGTL-----PSFSSTSPSPGTAIFRPEH 235
DB 154 DPCLPTLC-BENEMVKECTATSDAECRDLPWTHHTPSLAGSDSPETITRDPNTEG 212
QY 236 METHVPSSTVTPKGMNSTENSGAS-----VRPKVLSIQEGTVPDNTSSARGKEDVNKT 291
DB 213 MATTLADIVTTVMGSSQPVWGRGTADNLIPYVCISILAAVVGLVAYIAFKRWNSCKONKQ 272
QY 292 LPNLQVNVHQGHRRHLLKLPMEATGGSGSTPIKGRGHRPRONLKHKHDINEHLP 351
DB 273 GANRPVNTQTSPE-----GK-----LHSDSGI----- 296
QY 352 WNVILFLLLVIVVCSIRKSSRLTKGPRQDPSAIVEX--AGLKSMPTTQNRKWIY 409

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Db 297 -----SVDSSLDHQPPNOSTGDPAPKGDGSLYASLPSPKQEE----- 335
QY 410 YCNGHGIDILKLVAAGVGSQWKDIYQFLCNASEREVAAFSGY-----TADHERAYA 461
DB 336 -----VEKLSSABETWQL-----AGELGYKEDLDICFTREESPARA 374
QY 462 ALQHWITRGPASLAQLISALRQHRNDVVEKI 494
DB 375 LLADMSAK-ETATLDALLVALRKIQRGDIAESL 406

RESULT 11
TNFR_HUMAN
ID TNFR_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
DE (CD137 antigen).
GN TNFRSF9 OR ILA OR CD137.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand."
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family."
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand."
RL Immunol. Lett. 45:67-73(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Pearce A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7].
RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
RX MEDLINE=98078711; PubMed=9418902;
RA Arch R.H., Thompson C.B.;
RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve
growth factor receptor subfamily that bind TNF receptor-associated
factors and activate nuclear factor kappaB.";
RL Mol. Cell. Biol. 18:558-565 (1998).
RN [8].
RP INTERACTION WITH TRAF1 AND TRAF2.
RX MEDLINE=98270914; PubMed=9607925;
RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
RA Watts T.H.;
RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
4-1BB ligand.";
RL J. Exp. Med. 187:1849-1862 (1998).
RN [9].
RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX MEDLINE=21562677; PubMed=11804328;
RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in
4-1BB-mediated signal transduction.";
RL Mol. Cells 12:304-312 (2001).
CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
cell activation.
CC -!- SURUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with
LRR-repeat protein 1/LRR-1.
CC -!- TISSUE SPECIFICITY: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
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CC -----
DR EMBL; U03397; AAA53133.1; -.
DR EMBL; L12964; AAA62478.2; -.
DR EMBL; AL009183; CAB57398.1; -.
DR EMBL; BC006196; AAH06196.1; -.
DR PIR; I38426; I38426
DR Genew; HGNC:11924; TNFRSF9.
DR MIM; 602250; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 9.

FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT REPEAT 17 45
FT TNFR-CYS 1.
FT REPEAT 47 86
FT TNFR-CYS 2.
FT REPEAT 87 118
FT TNFR-CYS 3.
FT REPEAT 119 159
FT TNFR-CYS 4.
FT DOMAIN 214 255 INTERACTS WITH LRR-1.
FT DISULFID 28 37
FT BY SIMILARITY.
FT DISULFID 31 45
FT BY SIMILARITY.
FT DISULFID 48 62
FT BY SIMILARITY.
FT DISULFID 65 78
FT BY SIMILARITY.
FT DISULFID 88 94
FT BY SIMILARITY.
FT DISULFID 99 106
FT BY SIMILARITY.
FT DISULFID 102 117
FT BY SIMILARITY.
FT DISULFID 121 133
FT BY SIMILARITY.
FT DISULFID 139 158
FT BY SIMILARITY.
FT CARBOHYD 138 138
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;
Query Match 6.8%; Score 235.5; DB 1; Length 255;
Best Local Similarity 30.4%; Pred. No. 1.4e-08;
Matches 63; Conservative 24; Mismatches 77; Indels 43; Gaps 8;
QY 25 MIAGSLLLGFLSTTTAQPEQKASNLIGTYRHVDRTGQVLTCDCPKAGTYVSEHCNTS 84
DB 8 IVATLLLVLFNFRTRSLQD-----PCSNCPAGTF-----CDNNR 41
QY 85 LRVSSCPVGTFTFHENGIEKHCHDSQCPWPMEIKLPAAALTDRECTCPGPFQSNATC 144
DB 42 NQICSPCPNPSFS-SAGGORTDCIQ-QKGVFRTRKESSISNAECDCTPFCILGASC 99
QY 145 AP-HTVCPVGVGVKGTETEDVRCKQARGTFSDVPSSVMKCKAYTDCLSNVLVYKPG 203
DB 100 SMCEQDCKQQLTKKG-----CKDCFCGFNDQKRGII--CRPWTNCSLDGKSVLVNG 150
QY 204 TKETDNVCGTLPs-----FSSSTSPSP 225
DB 151 TKERDVVCGFSPADLSPGASSVTPFPAP 177
RESULT 12
TNRS MOUSE
ID TNRS_MOUSE STANDARD; PRT: 289 AA.
AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation.";
RJ J. Immunol. 148:620-626 (1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/c;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
RN [5]
RP FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RT LIGHT-mediated apoptosis of tumor cells.";
RL J. Biol. Chem. 275:14307-14315(2000).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664(1996).
RN [7]
RP INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA Gascoyne R.D., Berern K., McFadden D., Shabal A., Huh J.,
RA Reynolds A., Cleveland C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT adult, fetal, and tumor tissues.";
RL Am. J. Pathol. 152:1549-1561(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;

RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
CC -I- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNF514/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -I- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
CC EMBL; L04270; AAA36757.1; -;
CC EMBL; BC026262; AAA26262.1; -;
CC PIR; I54182; I54182.
CC HSPSP; P25942; ICDF.
CC Genew; HGNC:16718; LTR.
CC MIM; 600979; -;
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008063; Pas receptor.
CC InterPro; IPR001368; TNFR cf.
CC Pfam; PF00020; TNFR c6; 4;
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4;
CC PROSITE; PS00652; TNFR_NGFR_1; 2;
CC PROSITE; PS00505; TNFR_NGFR_2; 3;
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 624626B6022F656F CRC64;
Query Match 6.8%; Score 228.5; DB 1; Length 435;
Best Local Similarity 30.9%; Pred. No. 8.4e-08;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

QY 65 LTCDKCPAGTYVSEHTNTSLRYCSCPCVGTFTFRHENGIEKCHDCSQPC-PWPMEKL-P 122
Db 57 ICSCRPFGYIVSAKSRIDTVCATCAENSYNEHWNLTICQLC-RPCDPVWGLEIAP 115
QY 123 CAALTIRECTCTPPGFMFSNATCAPHTV-----CPVGVGVKRGKTETE----- 164
Db 116 CTSKRKTQCRQCPGMF-----CAAWALECTHCELLSDCP-----PGTEAEELKDEVGK 163
QY 165 DVRCQKQCARGTFSDFVSSVMKCKAYTDCLSQNLAVIKPGTKETDNCVGT-----LPFSSS 220

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Db 164 NNHCVPCKAGHPQNTSSPBARCQPHTRCENQGLVEARPTAQSDTTCKNPLEPLPPMSG 223
QY 221 T 221
Db 224 T 224

RESULT 14
ID TNRS_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
CC EMBL; U57745; AAC48710.1; -.
CC HSP; P25942; 1CDF.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00652; TNFR_NGFR_2; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 >269 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSFAM 194 215 SUPERFAMILY MEMBER 5.
FT DOMAIN 216 >269 EXTRACELLULAR (POTENTIAL).
FT REPEAT 25 60 CYTOPLASMIC (POTENTIAL).
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT DISULFID 26 37 TNFR-CYS 4.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 6.6%; Score 227; DB 1; Length 269;
Best Local Similarity 33.7%; Pred. No. 5.6e-08;
Matches 55; Conservative 17; Mismatches 65; Indels 26; Gaps 4;

QY 65 LTCDKCPAGTYVSEHCNTNTSLRVCSQPVGTTRHENGIEKCHD---CSQPCPWPMEK 121
Db 36 LCCLDPPGQKLVDCTEVSKTECSQSGKGFELSTWREKYCHEHRYCN----- 84
QY 122 PCAAL-----TDRECTCPGMFQSNAT---CAPHTVCPVGVKRGKGTETEDVCK 169
Db 85 PNLGURIQSEGLTNTDTICVVEGQCHTSHTCESTPHSLCLPFGVVKQIATGLLDTVCE 144
QY 170 QCARGTFSDVPSSVMKCKAYTDCLSQNLVVKPFGKTDNVCG 212
Db 145 PCPLGFFSNVSAFEKCHRWTSCKERGLVEQHVGTGKTDVVC 187

RESULT 15
ID VT2_MYXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor soluble receptor precursor (Protein T2).
GN M002L OR T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence";
RL Virology 184:370-382(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus.";
RL Virology 284:298-318(1999).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
CC EMBL; M95181; AAA46632.1; -.
CC DR EMBL; AF170726; AAF15046.1; -.
CC DR EMBL; AF170726; AAF14887.1; -.
CC DR EMBL; A23729; CAA01688.1; -.
CC DR PIR; A40566; QGVZML.
CC DR HSP; P19438; INCF.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00652; TNFR_NGFR_2; 2.
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Page 17

Search completed: September 21, 2004, 22:41:46
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:35:52 ; Search time 130 Seconds
(without alignments)
1589.726 Million cell updates/sec

Title: US-10-663-157-2
Perfect score: 3456
Sequence: 1 MGTSPSSSTALASCSRIARR.....SQBASQTLDVSVSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2715	78.6	573	11 Q8BZU6	Q8BZU6 mus musculus
2	2356	68.2	651	13 Q98SM6	Q98SM6 gallus gall
3	453	13.1	132	13 Q90Y18	Q90Y18 salvelinus
4	354	10.2	83	13 Q8UWJ0	Q8UWJ0 gallus gall
5	326.5	9.4	457	4 Q81VS6	Q81VS6 homo sapien
6	308	8.9	285	13 Q90W71	Q90W71 oncorhynch
7	307	8.9	285	13 Q90Y36	Q90Y36 oncorhynch
8	281.5	8.1	474	11 Q80WY6	Q80WY6 rattus norv
9	278	8.0	186	13 Q7ZZY5	Q7ZZY5 gallus gall
10	277	8.0	483	13 Q800K7	Q800K7 paralicthy
11	275.5	8.0	433	11 Q91ZM6	Q91ZM6 rattus norv
12	275.5	8.0	459	11 Q623Z7	Q623Z7 mus musculu
13	268.5	7.8	302	13 Q9PU50	Q9PU50 salvelinus
14	262.5	7.6	482	11 Q88734	Q88734 mus musculu
15	262	7.6	467	13 Q800I0	Q800I0 gallus gall
16	259.5	7.5	275	11 Q80WM9	Q80WM9 mus musculu

17	257	7.4	462	13 Q805B0	Q805B0 gallus gall
18	250	7.2	274	6 Q7YRL5	Q7YRL5 canis fami
19	248.5	7.2	167	12 Q8UYL3	Q8UYL3 vaccinia vi
20	248.5	7.2	167	12 Q72762	Q72762 cowpox viru
21	240.5	7.0	167	12 Q9DJL2	Q9DJL2 cowpox viru
22	240.5	7.0	318	13 Q7T2H3	Q7T2H3 encornynch
23	238	6.9	351	12 Q57117	Q57117 cowpox viru
24	237.5	6.9	360	12 Q57118	Q57118 cowpox viru
25	233	6.7	351	12 Q57121	Q57121 cowpox viru
26	232.5	6.7	347	12 Q57119	Q57119 cowpox viru
27	231	6.7	146	13 Q7ZZY4	Q7ZZY4 gallus gall
28	231	6.7	277	6 Q8WMQ2	Q8WMQ2 ovis aries
29	231	6.7	289	11 Q8K2X6	Q8K2X6 mus musculu
30	230.5	6.7	349	12 Q57100	Q57100 monkeypox v
31	230	6.7	348	12 Q57108	Q57108 monkeypox v
32	230	6.7	348	12 Q57277	Q57277 monkeypox v
33	230	6.7	348	12 Q57103	Q57103 monkeypox v
34	228.5	6.6	349	12 Q57102	Q57102 monkeypox v
35	228	6.6	347	12 Q57115	Q57115 cowpox viru
36	227.5	6.6	349	12 Q57101	Q57101 monkeypox v
37	227.5	6.6	349	12 Q57291	Q57291 monkeypox v
38	227	6.6	278	6 Q8SQ34	Q8SQ34 sus scrofa
39	226	6.5	317	13 Q8UFV6	Q8UFV6 brachydanio
40	225.5	6.5	349	12 Q57099	Q57099 monkeypox v
41	225	6.5	355	12 Q85308	Q85308 cowpox viru
42	223.5	6.5	350	12 Q57116	Q57116 cowpox viru
43	221.5	6.4	349	12 Q57305	Q57305 cowpox viru
44	216.5	6.3	326	12 Q57120	Q57120 cowpox viru
45	214.5	6.2	326	12 Q57122	Q57122 cowpox viru

ALIGNMENTS

RESULT 1

Q8BZU6 PRELIMINARY; PRT; 573 AA.

AC Q8BZU6; Q8BZU6; 23, Created)
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Death receptor 6.
GN TNFRSF21 OR AA959878.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466951;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK033529; BAC28342.1; -.
DR MGD; MGI:2151075; Tnfrcsf21.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SMC0005; DEATH; 1.
DR SMART; SMC0008; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 573 AA; 63506 MW; BC883B4EC8F2FE94 CRC64;

Query Match 78.6%; Score 2715; DB 11; Length 573;
Best Local Similarity 89.9%; Pred. No. 1.4e-218;

Matches 515; Conservative 16; Mismatches 40; Indels 2; Gaps 2;
 QY 84 SLRVCSSCPVGTTHRENGIEKCHDCSPCPWPMIEKLPALTDRECTCPGWFQSNAT 143
 DB 2 SLRVCSSCPAGTTHRENGIERCHDCSPCPWPMIERLPALTDRECTCPGMYQNGT 61
 QY 144 CAPHTVCPVGVGRKKGTTEDVRCQACARTGTFSDVSSVMKCKAYTDCLSONLVVILKPG 203
 DB 62 CAPHTVCPVGVGRKKGTTEDVRCQACARTGTFSDVSSVMKCKAHTDCLGONLEVVKPG 121
 QY 204 TKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHMETHEVPSSYVYVPGMNSSTESSSASVR 263
 DB 122 TKETDNVCGMRLFFSSTNPPSSGTVTFSSHPEMESHVPSFTYBPQGMNSTDSNSTASVR 181
 QY 264 KYLVSSIOEGTVDPNTSSARGKEDVNTLPLNLOVNHQOQPHRHILKLLP-SWEATGGE 322
 DB 182 TKVPSGIEEGTVDPNTSSGKEGNTNRTLPNPQVTHQAPPHRHILKLLPSSMEAT-GE 240
 QY 323 KSSTPIKPKRGHPRQNLKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLKKGPR 382
 DB 241 KSSTAIPKPKRGHPRQNAKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLKKGPR 300
 QY 383 QDPSAIVKAGLKKSWTQNTQNRKWIYYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASE 442
 DB 301 QDPSAIVKAGLKKSLTPTQNRKWIYYRNGHGIDILKLVAAQVGSQWKDIYQFLCNASE 360
 QY 443 REVAFAFNGYTADHERAYAAHQHTTIRGPEASLAQLISALQHRNDVVEKIRGLMEDTT 502
 DB 361 REVAFAFNGYTADHERAYAAHQHTTIRGPEASLAQLISALQHRNDVVEKIRGLMEDTT 420
 QY 503 QLETDKALPMSPLSPSPSPNAKLENSALLTVEPSPQDKNGKGFVDESEPLLRCD 562
 DB 421 QLETDKALPMSPLSPSPSPNVKLENSTLLTVEPSPDKNGKCFVDESEPLLRCD 480
 QY 563 TSSGSSALSNGSFTTKEKKOTVLRQVRLDPCDQPIFDMDLHLNPEELRVIEEIPQAE 622
 DB 481 TSSGSSALSNGSFTTKEKKOTVLRQVRLDPCDQPIFDMDLHLNPEELRVIEEIPQAE 540
 QY 623 DKLDRLFEIIGVKSEASQTLSDSVYSHLPDLL 655
 DB 541 DKLDRLFEIIGVKSEASQTLSDSVYSHLPDLL 573
 RESULT 2
 Q98SM6
 ID Q98SM6 PRELIMINARY; PRT; 651 AA.
 AC Q98SM6;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Death receptor 6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "Expression of DR6 in the ovary";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349908; AAK29666.2; --
 DR PIR; JC7705; JC7705.
 DR HSP; P19438; INCF.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS0050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;
 Query Match 68.2%; Score 2356; DB 13; Length 651;
 Best Local Similarity 70.9%; Pred. No. 2.1e-188; Indels 46; Gaps 10;
 Matches 470; Conservative 47; Mismatches 101;
 QY 23 ATMIAGSLLLGLSTTTAQP----EOKASNL-IGTYRHVDRATQVLTCDKCPAGTYS 77
 DB 3 AAVLAALVPLLVFLGTADAPKLTSEQNAVSLPAGKYLHLDRATQELICDKCPAGTYS 62
 QY 78 ECHTWTSLRVCSGCVGTTHRENGIEKCHDCSPCPWPMIEKLPALTDRECTCPGM 137
 DB 63 KCHTSTLRECSPCPDGTFTHRENGIERCHPCKPELFMIEKTHCTALTRECTCLSGT 122
 QY 138 FGSNATCAPHTVCPVGVGRKKGTTEDVRCQACARTGTFSDVSSVMKCKAYTDCLSONL 197
 DB 123 FQINTCVPTVCPVGVGRKKGTTEDVRCQACARTGTFSDVSSVMKCKAYTDCLSONL 182
 QY 198 VVIKGTGKTDVCG---TLP--SFSSSTSPSPGTAIFPRPEHMETHEVPSSYVYVPGMN 252
 DB 183 VVVKGTGKESNVCGSPASLPTSLTSSDAQDG-----ETYEAPPTAYLPKGLN 232
 QY 253 STESNSSASVRPKVLSSIOEGTVDPNTSSARGKEDVNTLPLNLOVNHQOQPHRHILKL 312
 DB 233 SVFLDSSSPAPRVNSGTAETVDTNDTSANGTVGAPQSLSSAGTAGQAQSYRKHSTQA 292
 QY 313 L---FSMEATGEGKSTPIKPKRGHPRQNLKHFDINEHLPWMIVLFLLLVLVIVVCS 369
 DB 293 MGKQPAQAEVAGGKSSIPYRPPRGPP--NVHQHFDINEHLPWMIVLFLLLVLVIVVCS 350
 QY 370 IRKSSRTLKKGPDPSPALVEKAGLKKSWTQNTQNRKWIYYCNGHGIDILKLVAAQVGSQ 429
 DB 351 VRKSSRTLKKGPDPSPALVEKAGLKKSWTQNTQNRKWIYYCNGHGIDILKLVAAQVGSQ 410
 QY 430 WKDIYQFLCNASEREVAFAFNGYTADHERAYAAHQHTTIRGPEASLAQLISALQHRND 489
 DB 411 WKDIYQFLCNASEREVAFAFNGYTADHERAYAAHQHTTIRGPEASLAQLISALQHRND 470
 QY 490 VVEKIRGLMEDTT-----QLETDKALPMSPLSPSPSPNAKLE 531
 DB 471 VVEKIRGLMEDTTVPVQMQPQVQDQCSNDGKGLALPVPSPSPSPVPTSP--KPP 528
 QY 532 NSALLTVEPSPQDKNGKGFVDESEPLLRCDSTSSGSSALSNGSFTTKEKKOTVLRQVRL 591
 DB 529 DAALVTVEPSPSEK-KCFVDESEPLLRCDSTSSGSSALSNGSFTTKEKKOTVLRQVRL 587
 QY 592 DPCDQPIFDMDLHLNPEELRVIEEIPQAEKLDRLFEIIGVKSEASQTLSDSVYSHL 651
 DB 588 DPCDQPIFDMDLHLNPEELRVIEEIPQAEKLDRLFEIIGVKSEASQTLSDSVYSHL 647
 QY 652 PDLL 655
 DB 648 PDLL 651
 RESULT 3
 Q90Y18
 ID Q90Y18 PRELIMINARY; PRT; 132 AA.
 AC Q90Y18;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Death receptor 6 (Fragment).
 GN DR6.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]


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RP SEQUENCE FROM N.A.
RA Bridgman J.T., Bobe J., Goetz F.W., Johnson A.L.;
RT "Conservation of Death Receptor-6 (DR6) in avian and piscine
RL vertebrates.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2001).
DR EMBL; AF302493; AAL09310.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 132
FT NON_TER 132
SQ SEQUENCE 132 AA; 14303 MW; B01FED44260CLEBS CRC64;

Query Match 13.1%; Score 453; DB 13; Length 132;
Best Local Similarity 56.1%; Pred. No. 5,2e-30;
Matches 74; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 74 TVVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQPCWPWMEIKLPAAALTDRECTC 133
Db 1 TVVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQPCWPWMEIKLPAAALTDRECTC 60
QY 134 PGMFQSNATCAPHTVCPVGMGVRKKGTEDEVCKQCARGTFSFDPSSVMKCKAYTDCL 193
Db 61 PPDFTQDSCSTAHSCLCPVSGVGRGNDVEDVCKACARGSFSDMASSVLRCRTHIDCL 120
QY 194 SQNLVVIKPGTK 205
Db 121 AQLPLLAAGTR 132

RESULT 4
Q8UWJ0 PRELIMINARY; PRT; 83 AA.
ID Q8UWJ0
AC Q8UWJ0;
DT 01-WAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Death receptor 6 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432512; AAL35560.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 83
FT NON_TER 83
SQ SEQUENCE 83 AA; 9506 MW; 28F8C880F655FADC CRC64;

Query Match 10.2%; Score 354; DB 13; Length 83;
Best Local Similarity 94.4%; Pred. No. 5,2e-22;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 434 YQFLCNASEREVAFNSGYTADHERAYAAALQHWITRGPASIAQLISALRQHRNDVVEK 493
Db 1 YQFLCNASEREVAFNSGYTADHERAYAAALQHWITRGPASIAQLISALRQHRNDVVEK 60
QY 494 IRGLMEDTTQLE 505
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Db 61 IRGLMEDTTQVQ 72

RESULT 5
Q8IVS6 PRELIMINARY; PRT; 457 AA.
ID Q8IVS6
AC Q8IVS6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 1B
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042167; AAR42167.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 457 AA; 48120 MW; 1B634BBF1F5D77AC CRC64;

Query Match 9.4%; Score 326.5; DB 4; Length 457;
Best Local Similarity 29.2%; Pred. No. 1.3e-18;
Matches 103; Conservative 38; Mismatches 125; Indels 87; Gaps 15;

QY 42 QPEQKASNLIGTVRHHVDRA---TGQVLTCDKCPA---GTVVSEHCTNTSLRVSCSPVGT 96
Db 23 QPDPARTH--GARRRLGRARRTG-ALGCGARLARFGQAKVFCIKTSDTVCDSCDSIV 79
QY 97 TRHENGIEKCHDCSQPCWPWMEIKLPAAALTDRECTCPGMF-----OSNATCAPHTVC 150
Db 80 TQLMNVVPECLSCGSRCSDDVETQACTREQNRICTCPFGWYCALSKQEGCLCAPLRKC 139
QY 151 FVGMGVRKKGTEDEVCKQCARGTFSFDPSSVMKCKAYTDCLSNLVVIKPKTKTDNV 210
Db 140 RPFQGVARPGTETSDVVCPCAPGTFSTNTSDTDCRPHQIC---NVVAL-PGNASNDV 195
QY 211 CGTLPFSSTSP-----SFGTAIFRPP-----EKMETHVPS-----STVVPKGMNSTES 256
Db 196 C-----TSTSPTRSMAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSLPMPGSPRAE 248
QY 257 NSS-----ASVYPKVLSSIQEGTVPD--NTSSARGKE 286
Db 249 GSTGDFALPVGLIVGVTALGLIIGVNVNVTQVKKPLCLQREAKVPHLPADKARG-- 306
QY 287 DVNKTLPNLQVNVHQHRRHILKLLPSMEATGCKSKSTPI--KGPKRGHPR 337
Db 307 -----TQPEQQLLIITAPSSSSSSLESSASALDRRAPTRNQFQ 345

RESULT 6
Q90W71 PRELIMINARY; PRT; 285 AA.
ID Q90W71
AC Q90W71;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RA Pleguezuelos O.; Secombes C.J.;
 RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ315137; CAC43329.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS01186; EGF 2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;
 Query Match 8.9%; Score 308; DB 13; Length 285;
 Best Local Similarity 35.6%; Pred. No. 2.3e-17;
 Matches 67; Conservative 22; Mismatches 79; Indels 20; Gaps 3;
 QY 53 TYRHVDRTGQVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQP 112
 DB 30 TYWRDDATGDSLTCDLCPAGTYLLKHCTKORKSDCGPCPKSHYTEIWNHYERQYCNRF 89
 QY 113 CPWPMIEKLPCAAALDRECTCPGFMFQSNATCAHTVCPVGMGVRKKGTTETEDVRCKQCA 172
 DB 90 CTADIESVPTQLNRCQCKDGFYMTGSCSRHRCPPGEGVISNGTAHTDVKCEPCP 149
 QY 173 RGTFSDPVSSVMKXAYTDCLSNLVIKPGTKETDNCV 211
 DB 150 VGFFSAVSSSRKACQKFSVCPGGRTTI--PGNDMNDVYC 186
 RESULT 8
 Q90YS6 PRELIMINARY; PRT; 285 AA.
 AC Q90YS6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2003 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TNF decoy receptor.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
 RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
 RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
 RT fragments containing AU-rich elements."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF491631; AAK91758.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS01186; EGF 2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;

Query Match 8.9%; Score 307; DB 13; Length 285;
 Best Local Similarity 38.4%; Pred. No. 2.7e-17;
 Matches 61; Conservative 20; Mismatches 76; Indels 2; Gaps 1;
 QY 53 TYRHVDRTGQVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQP 112
 DB 30 TYWRDDATGDSLTCDLCPAGTYLLKHCTKORKSDCGPCPKSHYTEIWNHYERQYCNRF 89
 QY 113 CPWPMIEKLPCAAALDRECTCPGFMFQSNATCAHTVCPVGMGVRKKGTTETEDVRCKQCA 172
 DB 90 CTADIESVPTQLNRCQCKDGFYMTGSCSRHRCPPGEGVISNGTAHTDVKCEPCP 149
 QY 173 RGTFSDPVSSVMKXAYTDCLSNLVIKPGTKETDNCV 211
 DB 150 VGFFSAVSSSRKACQKFSVCPGGRTTI--PGNDMNDVYC 186
 RESULT 8
 Q80WY6 PRELIMINARY; PRT; 474 AA.
 AC Q80WY6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor receptor type II.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kistritz; TISSUE=Spleen;
 RA Li Y., Ji A., Schaefer M.K.;
 RT "Expression of TNFR2 in rat dorsal root ganglion."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF498039; AAP33151.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 3.
 KW Receptor.
 SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;
 Query Match 8.1%; Score 281.5; DB 11; Length 474;
 Best Local Similarity 25.9%; Pred. No. 7.9e-15;
 Matches 83; Conservative 39; Mismatches 128; Indels 71; Gaps 11;
 QY 65 LTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQPCPMPMIEKLPCA 124
 DB 53 MCCAKCPGQYAKHFCNKTSDTVCAACAGMFTQVMNHLHTCLSCSSCSDQVETHNCT 112
 QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGMGVRKKGTTETEDVRCKQARGTFS 177
 DB 113 KQKNRYVCACNADSYCALXHLHSGNCQCKMLSCGPGFGVARSNTSGNIVCSACAPGTFS 172
 QY 178 DVPSSVMKXAYTDCLSNLVIKPGTKETDNCVCTLPFSFSSSTSPS--PGTAIFPRPE- 234
 DB 173 DTTSSTDVCRPHRIC-----SILAIFGNASTDAVCA-----SESPTPSAVPTIVSQPEP 223
 QY 235 ----HMETEVEPSST-YVPKGNMST---ESNSASV----- 262
 DB 224 TRSQPMDOEPGPGSQTPHIPVSLGSPITPEISITGGISLPIGLIVLTLGLMLGLANCF 283
 QY 263 ----RPKVLSSIQEGTVDPDNTSSARGKEDVKNLTLENLQVNHQOQPHRHILKLLPSMEA 318
 DB 284 ILVQKKKPSCLQRETVMVPHLPDDKSDQAI-----GLEQQLLTITAPSSSS 329
 QY 319 TGGEKSSST--PIKGPGRGHRP 337
 DB 330 SSLESSASAGDRRAPPGGHPQ 350

the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.;

RT BLol. Reprod. 62:420-426 (2000).

RL EMBL; AF156738; AAD56428.1; -.

DR HSSP; O14763; 1D4V.

DR GO; 0004872; F:receptor activity; IEA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS01186; EGF 2; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 1.

KW Receptor.

SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.8%; Score 268.5; DB 13; Length 302;

Best Local Similarity 32.5%; Pred. No. 5e-14;

Matches 53; Conservative 26; Mismatches 81; Indels 3; Gaps 2;

QY 53 TYRHVDRATGQVLTCDCPCAGTYVSEHCTNTSLRVCSSCPVGTTRHENGIEKCHDCSQP 112

DB 22 TFKNDDRVGLSIVCDRCPPGTIRAPCSAMRKSDCACFPNGAYTFWNHLSKLCRCSM- 80

QY 113 CPWPMIEKLPCAAALTDRECTCPGGMF--QSNATCAPHTVCPVGVGRKKGTTETEDVRCKQ 170

DB 81 CAENQVVKQCSNNECECKEGYFNKYKVEACIKHKECPGPGYANTGTGPHQDTECVQ 140

QY 171 CARGTFSDVPSSVMKCKAYTCLSQLNVVIRKPGTKETDNCVT 213

DB 141 COAGFYSESSAKATCLAQSNCKVGLRLVILKQGDWHNLCLAS 183

RESULT 14

O88734 PRELIMINARY; PRT; 482 AA.

ID O88734

AC O88734

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE P80 TNF-alpha receptor.

GN TNFR2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96414512; PubMed=9740674;

RA Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;

RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure

RT and Characterization of the two Transcripts.";

RL Genomics 52:79-98 (1998).

DR EMBL; Y14619; CAA74969.1; -.

DR EMBL; Y14620; CAA74969.1; JOINED.

DR EMBL; Y14621; CAA74969.1; JOINED.

DR EMBL; Y14622; CAA74969.1; JOINED.

DR EMBL; Y14623; CAA74969.1; JOINED.

DR EMBL; Y14679; CAA74969.1; JOINED.

DR HSSP; O92956; 1JVA.

DR GO; 0004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS50050; TNFR_NGFR_2; 3.

KW Receptor.

SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 7.6%; Score 262.5; DB 11; Length 482;

Best Local Similarity 24.4%; Pred. No. 3.2e-13;

Matches 82; Conservative 33; Mismatches 128; Indels 93; Gaps 11;

QY 65 LTCDCPCAGTYVSEHCTNT-----SLRVCSSCPVGTTRHENGIEKCHDCSQPCPWPM 117

DB 53 MCCACPPQGYVKKFNKTSKSDTVCADCSASY:YQVWQFRTCLSCSSCSSTDO 112

QY 118 IEKLPCAAALTDRECTCPGGMFQSNAT-----CAPHTVCPVGVGRKKGTTETEDVRCKQ 170

DB 113 VETRACTKQNRVCAACEAGRYCALKTHSGSCRCQMLSKCGPGFGVASSRAPNGNVLCRA 172

QY 171 CARGTFSDVPSSVMKCKAYTCLSQLNVVIRKPGTKETDNCVTLSFSSSTSPSPCTAIF 230

DB 173 CAPGTFSDTTSSTVCRPHRIC-----SILAIFGNASTDAVCA----- 210

QY 231 PRPEHMETHEVPSSTYV-----PKGMNSTESNSASVRPKVLSSIOEGTVDPDNTSSARGKE 286

DB 211 --PESPTLSAIRTLVVSQPEPTRSQPLDQEPGQTPSILTSL--GSFTPIEQSTKG-- 264

QY 287 DVNKTLP-----NLQVNV-----HQQGP----- 305

DB 265 --GISLFIGLIVGTVSLGLMLGLVNCFLVQRKKPSCLOORDAKVPHVPDEKSDAVGL 322

QY 306 -HRHILKLPSMEATGEXSSTPI---KGPKEGHPR 337

DB 323 EQHLLTAPSSSSSSSSSSSSSASAGDRRAPPGGHQ 358

RESULT 15

O80010 PRELIMINARY; PRT; 467 AA.

ID O80010

AC O80010

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE CD30 protein precursor.

GN CD30.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Burgess S.C.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Burgess S.C.;

RL Thesis (1998); Bristol University, U.K.

DR EMBL; AJ276964; CAC79223.1; -.

DR GO; 0004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 3.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS50050; TNFR_NGFR_2; 1.

KW Signal.

FT SIGNAL.

FT CHAIN

SQ SEQUENCE 467 AA; 51350 MW; F9AD4F77DEEC8588 CRC64;

Query Match 7.6%; Score 262; DB 13; Length 467;

Best Local Similarity 29.0%; Pred. No. 3.3e-13;

Matches 86; Conservative 36; Mismatches 129; Indels 46; Gaps 12;

QY 11 LASCRIARRATATMIAGSLLILGLFSTTTA-OPEQKASNLIGTYRH--VDRATGQVLIC 67

DB 1 MASCS-----LRLGLWLLLLLODIOGAPQPTTSHSCDTLKNWYDETGLR--CC 49

QY 68 DKCPAGTYVSEHCTNTSLRVCSSCPVGTTRHENGIEKCHDCSQPC--PWPMIEKLPCAA 125

DB 50 YQCPSGYAKKSCPMDEDCNRCGEQYL-NQSPKPCDACVL-CTKEFDLVEKAPCSF 107

QY 126 LTIRECTCPGGMFQSNAT-----CAPHTVCPVGVGRKKGTTETEDVRCKQCARGTFSDV 179

Db 108 NSSRVCECPGMFCQTAANKTCMRQHTACKPGFVKIRGTSETDVSCECPGTFSDQ 167
Qy 180 PSSVMKCKAYTDCLSQNLVVIKPGTKETDNVC-GTLPSPSSSTSPSPGTAIFPRPEHMET 238
Db 168 SSSTDVCKPHTDCAKLNKVAQCKGNATHDQVCTDQPSYL-----TPDTSSI-----RIT 217
Qy 239 HEVPSSTYVPKGMNSTEGNSSASVRPKVLSIIQEGTVPDNTSSARGKEDVNKTLPLNL 295
Db 218 NETDSDVLKRAN-----PVTLASILSSATTEIPGSTPEEALAGTSPTL 263

Search completed: September 21, 2004, 22:44:03
Job time : 133 secs